	L #	Hits	Search Text	DBs	Time Stamp
1	L1	20	arginine adj methyltransferase$1	USPAT; US-PGPUB	2003/07/31 10:27
2	L2	2265	(steroid or glucocorticoid) adj receptor$1	USPAT; US-PGPUB	2003/07/31 10:28
3	L3	12574	transcription$ near6 (activat$8 or coactivat$8)	USPAT; US-PGPUB	2003/07/31 10:28
4	L4	81	(2 or 3) same methyltransferase$1	USPAT; US-PGPUB	2003/07/31 10:29
5	L5	96	1 or 4	USPAT; US-PGPUB	2003/07/31 10:29

PGPUB-DOCUMENT-NUMBER: 20030135032

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030135032 A1

TITLE: Methods and compositions for bioremediation

PUBLICATION-DATE: July 17, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 10/ 181319

DATE FILED: October 1, 2002

PCT-DATA:
APPL-NO: PCT/US01/02386
DATE-FILED: Jan 19, 2001
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 536/23.1, 435/252.3 , 435/320.1

ABSTRACT:

The present invention provides isolated nucleic acid molecules that encode one or more of the enzymes required to produce PDTC. The present invention also provides isolated proteins encoded by nucleic acid molecules of the invention. In another aspect, the present invention provides methods for reducing the amount of a metal in a substrate, such as soil. In yet another aspect, the present invention provides methods for reducing the amount of carbon tetrachloride in a substrate, such as soil.

---------- KWIC ---------

Detail Description Table CWU - DETL (3):
3TABLE 3 Putative open reading frames (RFs) encoded within the pT31 insert (SEQ ID NO: 13). ORF/ SEQ ID Start Ending NO: Base Base AA kDa pI Homology A/30 1 360 >119 >13.8 NA Similar to acyl-CoA synthase from

Mycobacterium bovis (AAB52538); BLOSUM62 expect = 5 .times. 10.sup.-10, 36% identities and 53% positives over 121 aa overlap. B/22 158 1099 313 34.2 10.39 Probable thioesterase. Similar to gramicidin S biosynthesis GRST protein from Brevibacillus brevis (P14686); BLOSUM62 expect = 3 .times. 10.sup.-23, 35% identities and 49% positives over 188 aa overlap. C/7 4066 3353 235 26.2 9.88 Probable **transcriptional activator.** Similar to XylS/AraC **transcriptional activator** from Salmonella typhimurium (3094022); BLOSUM62 expect = 2 .times. 10.sup.-9, 31% identities and 50% positives over 107 aa overlap. Has 25% identities and 50% positives to 40 aa AraC bacterial regulatory protein family protein signature (PROSITE PS00041). D/24 4486 5052 188 20.1 8.64 No significant homology. E/26 5187 6302 371 40.3 11.13 No significant homology. Has 11 predicted transmembrane domains. F/14 6475 7650 391 43.7 4.88 Possible sulfurylase. Similar to MoeZ from Mycobacterium tuberculosis (CAB08310); BLOSUM62 expect = 10.sup.-122, 57% identities and 71% positives over 388 aa overlap. Has a single predicted transmembrane domain located between residues 43 to 65. G/9 7666 8076 136 15.6 6.68 Similar to hypothetical 16.5 kd protein RV1334 precursor from Mycobacterium tuberculosis (Q10645); BLOSUM62 expect = 8 .times. 10.sup.-30, 47% identities and 67% positives over 134 aa overlap. H/11 8139 8411 90 9.7 5.61 Similar to hypothetical protein from Streptomyces coelicolor A3 (CAB50992); BLOSUM62 expect = 6 .times. 10.sup.-21, 48% identities and 74% positives over 90 aa overlap. Lower homologies to MoaD proteins. I/18 8446 10332 628 67.5 6.98 Similar to putative racemase from Rhodococcus sp. (CAB55821); BLOSUM62 expect = 2 .times. 10.sup.-23, 30% identities and 44% positives over 285 aa overlap. J/16 10278 12023 581 62.8 5.51 Probable AMP ligase. Similar to 2,3-dihydroxybenzoate-AMP ligase from Bacillus subtilis (P40871); BLOSUM62 expect = 3 .times. 10.sup.-50 , 28% identities and 45% positives over 529 aa overlap. Has AMP binding motif between residues 211-222. K/1 11974 14037 687 75.3 5.93 Probable receptor precursor. Similar to FyuA precursor from Escherichia coli (CAA84488); BLOSUM62 expect = 2 .times. 10.sup.-29, 25% identities and 40% positives over 586 aa overlap. Has 25 aa signal peptide located at amino terminus. Has TonB-dependent receptor protein signature (PROSITE PS00430). L/28 14069 16300 743 83.3 7.50 No significant homologies. M/30 16716 19010 764 83.0 6.09 Probable aminotransferase. Similar to SC6A5.18 from Streptomyces coelicolor (CAB39702); BLOSUM62 expect = 4 .times. 10.sup.-70, 34% identities and 50% positives over 467 aa overlap. N/3 19073 20251 392 40.6 10.72 Probable ABC transporter. Similar to YycB from Bacillus subtillis (CAB16085); BLOSUM62 expect = 5 .times. 10.sup.-9, 24% identities and 41% positives over 325 aa overlap. O/32 23041 21500 513 57.4 8.78 Probable acyl-CoA dehydrogenase. Similar to DR0922 from Deinococcus radiodurans; BLOSUM62 expect = 1 .times. 10.sup.-70, 38% identities and 58% positives over 386 aa overlap. P/5 23969 22914 351 38.2 5.82 Probable **methyltransferase.** Similar to hydroxyneurosporene **methyltransferase** (CrtF) from Rhodobacter sphaeroides CRTF_RHOSH); BLOSUM62 expect = 1 .times. 10.sup.-9, 30% identities and 40% positives over 204 aa overlap. Has 67% identities to S-adenosylmethionine- dependent **methyltransferase** motifs (Kagan and Clarke, 1994). Q/34 25588 25746 >53 >6.4 NA Similar to predicted coding region AF1178 (AAB90082) from Archaeoglobus fulgidus; BLOSUM62 expect = 2 .times. 10.sup.-4, 45% identities and 74% positives over 36 aa overlap.

PGPUB-DOCUMENT-NUMBER: 20030134350

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030134350 A1

TITLE: Zinc finger domain recognition code and uses thereof

PUBLICATION-DATE: July 17, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Sera, Takashi	San Diego	CA	US	

APPL-NO: 09/ 911261

DATE FILED: July 23, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60220060 20000721 US

US-CL-CURRENT: 435/69.1, 435/226 , 435/320.1 , 435/325 , 435/91.2 , 536/23.2

ABSTRACT:

The present invention relates to DNA binding proteins comprising zinc finger domains in which two histidine and two cysteine residues coordinate a central zinc ion. More particularly, the invention relates to the identification of a context-independent recognition code to design zinc finger domains. This code permits identification of an amino acid for positions -1, 2, 3 and 6 of the .alpha.-helical region of the zinc finger domain from four-base pair nucleotide target sequences. The invention includes zinc finger proteins (ZFPs) designed using this recognition code, nucleic acids encoding these ZFPs and methods of using such ZFPs to modulate gene expression, alter genome structure, inhibit viral replication and detect alterations (e.g., nucleotide substitutions, deletions or insertions) in the binding sites for such proteins. In addition, the invention provides a rapid method of assembling a ZFP with three or more zinc finger domains using three sets of 256 oligonucleotides, where each set is designed to target the 256 different 4-base pair targets and allow production of all possible 3-finger ZFPs (i.e., >>10.sup.6) from a total of 768 oligonucleotides.

[0001] This application claims benefit of co-pending, provisional application U.S. Serial No. 60/220,060, filed Jul. 21, 2000.

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Summary of Invention Paragraph - BSTX (37):

[0033] In a particular embodiment, a fusion protein has a first segment which is any ZFP of the invention, and a second segment comprising a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator,** a single-stranded DNA binding protein, a nuclear-localization signal, a transcription-protein recruiting protein or a cellular uptake domain. In an alternative embodiment, the second segments can comprise a protein domain which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear localization activity, transcriptional protein recruiting activity, **transcriptional repressor activity or transcriptional activator** activity.

Detail Description Paragraph - DETX (37):

[0125] In addition, the invention includes isolated fusion proteins comprising a ZFP of the invention fused to second domain (an effector domain) which is a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator, single-stranded DNA binding protein, transcription** factor recruiting protein nuclear-localization signal or cellular uptake signal. In an alternative embodiment, the second domain is a protein domain which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear-localization signaling activity, **transcriptional repressor activity, transcriptional activator** activity, single-stranded DNA binding activity, transcription factor recruiting activity, or cellular uptake signaling activity.

Detail Description Paragraph - DETX (109):

[0195] Likewise an effector domain can include, but is not limited to a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator,** a single-stranded DNA binding protein, a nuclear-localization signal, a transcription-protein recruiting protein or a cellular uptake domain. Effector domains further include protein domains which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear localization activity, transcriptional protein recruiting activity, **transcriptional repressor activity or transcriptional activator** activity.

PGPUB-DOCUMENT-NUMBER: 20030134318

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030134318 A1

TITLE: Methods of using randomized libraries of zinc finger proteins for the identification of gene function

PUBLICATION-DATE: July 17, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 337216

DATE FILED: January 6, 2003

RELATED-US-APPL-DATA:

child 10337216 A1 20030106

parent continuation-of 09731558 20001206 US GRANTED

parent-patent 6503717 US

child 09731558 20001206 US

parent continuation-in-part-of 09456100 19991206 US ABANDONED

US-CL-CURRENT: 435/6, 435/7.1

ABSTRACT:

The present invention relates to methods of using libraries of randomized zinc finger proteins to identify genes associated with selected phenotypes.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Ser. No. 09/456,100, filed Dec. 6, 1999, herein incorporated by reference in its entirety.

[0002] This application is related to U.S. Ser. No. 09/229,007, filed Jan. 12, 1999, and U.S. Ser. No. 09/229,037, filed Jan. 12, 1999, and U.S. Ser. No. 09/395,448, filed Sep. 14, 1999, herein each incorporated by reference in their entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (7):
[0039] In one embodiment, the zinc finger protein is linked to at least one or more regulatory domains, described in detail below. Preferred regulatory domains include **transcription factor repressor or activator** domains such as KRAB and VP 16, co-repressor and co-activator domains, DNA **methyltransferases,** histone acetyltransferases, histone deacetylases, and endonucleases such as Fok1. For repression of gene expression, often simple steric hindrance of transcription initiation is sufficient.

Detail Description Paragraph - DETX (24):
[0056] A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (61):
[0093] Common regulatory domains for addition to the zinc finger protein include, e.g., eftector domains from **transcription factors (activators,** repressors, co- activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20030134302

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030134302 A1

TITLE: Libraries of expressible gene sequences

PUBLICATION-DATE: July 17, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 210985

DATE FILED: August 1, 2002

RELATED-US-APPL-DATA:

child 10210985 A1 20020801

parent continuation-of 10003021 20011114 US PENDING

child 10003021 20011114 US

parent continuation-of 09285386 19990402 US ABANDONED

non-provisional-of-provisional 60096981 19980818 US

non-provisional-of-provisional 60080626 19980403 US

US-CL-CURRENT: 435/6, 435/320.1 , 435/325 , 435/69.1 , 536/23.2

ABSTRACT:

The invention described herein comprises libraries of expressible gene sequences. Such gene sequences are contained on plasmid vectors designed to endow the expressed proteins with a number of useful features such as affinity purification tags, epitope tags, and the like. The expression vectors containing such gene sequences can be used to transfect cells for the production of recombinant proteins. A further aspect of the invention comprises methods of identifying binding partners for the products of such expressible gene sequences.

RELATED APPLICATIONS

[0001] This application relies for priority on U.S. Provisional Application No. 60/080,626, filed Apr. 3, 1998, and U.S. Provisional Application No.

60/096,981, filed Aug. 18, 1998, each of which is hereby incorporated herein in its entirety.

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Detail Description Table CWU - DETL (51):

protein phosphatase 2C alpha 42.13 52.0 kDa [human, teratocarcinoma, mRNA, 2346 nt] M472 B1 H-U00803 tyrosine-protein kinase FRK 55.620 64.0 kDa B2 H-U02390 Human adenylyl cyclase- 52.58 55 associated protein homolog CAP2 (CAP2) mRNA, complete cds 167-2 H-U02680 human protein tyrosine kinase 36 38.57 mRNA G2 H-U03056 Human tumor suppressor (LUCA- 47.96 47 1) mRNA, complete cds M512 E3 H-U03100 Human alpha2(E)-catenin mRNA, 102.52 102.0 kDa complete cds M306 G3 H-U03187 72.93 95.0 kDa H3 H-U03398 Human receptor 4-1BB ligand 28.05 51 mRNA, complete cds D3 H-U03486 Human connexin40 gene, 39.49 40 complete cds M300 C3 H-U03643 leukophysin 25.96 34 F5 H-U03749 Human chromogranin A (CHGA) 50.38 50 gene, promoter and M314 C3 H-U03886 GS2 (GB: U03886) 27.94 32.0 kDa M306 E3 H-U04343 CD86 antigen (CD28 antigen 35.64 47 ligand 2, B7-2 antigen) [CD86] 167-61 H-U05012 TrkC 92 90.82 M302 G5 H-U05340 cell division cycle protein p55 55 55 A4 H-U05659 Hydroxysteroid (17-beta) 34.21 36 dehydrogenase 3 F1 H-U05861 Human hepatic dihydrodiol 35.64 40 dehydrogenase gene M302 B2 H-U06452 antigen MART-1, melanoma 13.09 20.0 kDa 169-52 H-U06454 human AMP-activated protein 70 60.79 kinase (hAMPK) mRNA M315 A3 H-U06643 lectin, epidermal 15.07 18 H1 H-U06715 Cytochrome B561 27.06 25 M476 E5 H-U07132 Human steroid hormone receptor 50.82 55.0 kDa Ner-l mRNA, complete cds M236 D3 H-U07151 guanine nucleotide-binding 20.13 34 protein ADP-ribosylation factor like gene 3 M317 G3 H-U07559 homeotic protein Islet-1 38.17 38 M266 H1 H-U07681 Human NAD(H)-specific 40.37 40 isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds E3 H-U07919 Aldehyde dehydrogenase 6 56.43 53 M298 A3 H-U08021 nicotinamide N-**methyltransferase** 29.15 36.0 kDa M297 B1 H-U08024 alcohol/hydroxysteroid 31.46 50.0 kDa sulfotransferase A2 H-U08336 Human basic helix-loop-helix 21.89 42 transcription factor mRNA, complete cds E2 H-U09303 Human T cell leukemia LERK-2 38.17 40 (EPLG2) mRNA, complete cds M250 H5 H-U09559 RCH1, RAG (recombination 58.3 58.0 kDa activating gene) cohort 1 167-50 H-U09564 human serine kinase mRNA 72 72.12 166-74 H-U09578 human MAPKAP kinase (3pK) 50 42.09 mRNA M302 C4 H-U09813 ATP synthase, subunit 9, 15.73 30 mitochondrial A1 H-U09850 Zinc finger protein 143 (clone 68.97 68 pHZ-1) M423 E1 H-U09937 Human urokinase-type 36.96 49.0 kDa plasminogen receptor M450 H4 H-U10117 Human endothelial-monocyte 34.43 38.0 kDa activating polypeptide II mRNA, complete cds M314 G1 H-U10248 ribosomal protein L29 17.6 27 M298 H1 H-U10323 nuclear factor 45 44.77 45 E1 H-U10492 Human Mox1 protein (MOX1) 28.05 37 mRNA, complete cds F3 H-U10686 Human MAGE-11 antigen 35.2 35 (MAGE11) gene, complete cds 167-38 H-U11050 human NIMA-like protein kinase 55 49.02 1 (NLK1) mRNA M266 B2 H-U11292 Human Ki nuclear autoantigen 29.48 32 mRNA, complete cds, may play a rol in cell adhesion 167-62 H-U11791 human cyclin H mRNA 40 35.60 M423 D5 H-U12255 immunoglobulin gamma heavy 40.26 48.0 kDa chain Fc receptor RI, high affinity M302 F7 H-U12404 Csa-19 23.98 32 M236 A2 H-U12465 ribosomal protein L35 13.64 24 169-4 H-U12535 human epidermal growth factor 100 90.49 receptor kinase substrate (Eps8) mRNA F3 H-U12597 Human tumor necrosis factor type 55.22 64 2 receptor associated protein (TRAP3) mRNA, complete cds M314 D1 H-U12979

transcriptional coactivator PC4 14.08 23 M476 G4 H-U13044 GA-binding protein transcription 50.05 53.0 kDa factor, alpha subunit (60 kD) M302 F3 H-U13665 cathepsin O (GB: U13665) 36.3 50.0 kDa M311 G4 H-U13831 cellular retinol binding protein II 14.85 20.0 kDa A2 H-U13991 Human TATA-binding protein 24.09 34 associated factor 30 kDa subunit (tafII30) mRNA, complete cds M416 A4 H-U14187 Human receptor tyrosine kinase 26.29 29.0 kDa ligand LERK-3 (EPLG3) mRNA, complete cds M250 A2 H-U14188 eph-related receptor tyrosine 22.22 27 kinase ligand 4 [EPLG4] M302 D2 H-U14193 human TFIIA gamma subunit 12.060 28.0 kDa mRNA M416 G1 H-U14603 Human protein-tyrosine 18.48 30.0 kDa phosphatase (HU-PP-1) mRNA, partial sequence E2 H-U14747 Visinin-like 1 21.12 25 M266 D4 H-U14966 ribosomal protein L5 32.78 38 M314 E2 H-U14967 ribosomal protein L21 17.71 29 M266 F5 H-U14968 ribosomal protein L27a 16.39 19.0 kDa M248 E3 H-U14969 ribosomal protein L28 15.18 27 M266 E1 H-U14971 ribosomal protein S9 21.45 30 M250 C2 H-U15009 small nuclear ribonucleoprotein, 13.97 17.0 kDa Sm D3 M311 D4 H-U16660 enoyl-Coenzyme A hydratase-like 36.19 38 protein, peroxisomal M302 H4 H-U17074 cyclin-dependent kinase 6 18.59 29 inhibitor p18 M306 A2 H-U17195 A-kinase anchor protein 100 72.05 100 [AKAP100*] D1 H-U17280 Steroidogenic acute regulatory 31.46 35 protein M316 F1 H-U18291 cell division cycle protein 16 68.2 71.0 kDa C5 H-U18420 Human ras-related small GTP 23.87 33 binding protein Rab5 (rab5) mRNA, complete cds M311 A2 H-U18423 spinal muscular atrophy gene 32.45 41 M248 D4 H-U18914 hypothetical protein, (Human 20.35 32 19.8 kDa protein mRNA, complete cds) M302 B5 H-U19718 microfibril-associated 20.24 34.0 kDa glycoprotein 2 M305 E3 H-U20240 CCAAT/enhancer-binding protein 16.61 29 gamma M302 A8 H-U20352 malate dehydrogenase 36.85 40 M416 F4 H-U20391 Human folate receptor (FOLR1) 28.38 34.0 kDa gene, complete cds M311 D1 H-U20536 apoptotic cysteine protease Mch2 32.34 38.0 kDa M431 G2 H-U20659 RNA polymerase II, subunit B7 19.03 31.0 kDa M499 C1 H-U20938 Human lymphocyte 112.86 100.0 kDa dihydropyrimidine dehydrogenase mRNA, complete cds M305 F2 H-U20972 14-3-3 protein, epsilon 28.16 36 M271 D3 H-U21049 hypothetical protein 12.65 16 (GB: U21049), ESTs, Highly similar to DD96 [H. sapiens]. M421 G5 H-U21858 Human **transcriptional activation** 29.15 38.0 kDa factor TAFII32 mRNA, complete cds M424 H3 H-U22662 Human nuclear orphan receptor 49.28 49.0 kDa LXR-alpha mRNA, complete cds M271 D2 H-U24074 killer cell inhibitory receptor 37.62 43 [KIR], Homo sapiens natural killer-associated transcript 3 (NKAT3), complete cds. RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES. 169-29 H-U24153 human p21-activated protein 60 57.82 kinase (Pak2) gene M385 H2 H-U24166 EB1 29.59 36.0 kDa G1 H-U24169 Human JTV-1 (JTV-1) mRNA, 34.43 40 complete cds E1 H-U24576 Human breast tumor autoantigen 18.26 27 mRNA, complete sequence G4 H-U24577 Human LDL-phospholipase A2 48.62 52 mRNA, complete cds H1 H-U25789 Human ribosomal protein L21 17.71 32 mRNA, complete cds M416 D1 H-U25849 Human red cell-type low 17.49 28.0 kDa molecular weight acid phosphatase (ACP1) gene, 5' flanking region and M300 A3 H-U26312 heterochromatin protein H-P1Hs- 19.14 30 gamma M416 D3 H-U26403 Human receptor

PGPUB-DOCUMENT-NUMBER: 20030134280

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030134280 A1

TITLE: Identifying drugs for and diagnosis of benign prostatic hyperplasia using gene expression profiles

PUBLICATION-DATE: July 17, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Munger, William E.	Gaithersburg	MD	US	
Kulkarni, Prakash	Gaithersburg	MD	US	
Getzenberg, Robert H.	Pittsburgh	PA	US	
Waga, Iwao	Yokohama		JP	
Yamamoto, Jun	Yokohama		JP	

APPL-NO: 09/ 960706

DATE FILED: September 24, 2001

RELATED-US-APPL-DATA:

child 09960706 A1 20010924

parent continuation-in-part-of 09873319 20010605 US PENDING

non-provisional-of-provisional 60223323 20000807 US

US-CL-CURRENT: 435/6, 702/20

ABSTRACT:

The present invention is based on the elucidation of the global changes in gene expression in prostate tissue isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue as well as the identification of individual genes that are differentially expressed in diseased prostate tissue.

RELATED APPLICATIONS

[0001] This application claims priority of U.S. Provisional Application No. 60/223,323, filed Aug. 7, 2000, and U.S. application Ser. No. 09/873,319, filed Jun. 5, 2001, which are herein incorporated by reference in their entirety.

---------- KWIC ---------

Detail Description Table CWU - DETL (11):

4TABLE 4 Normal vs. BPH W/Symptoms Table (Down-regulated) SEQ ID Fold-Affymetrix element NO: GenBank ID GenBank Name change t rc_T40895_at 892 T40895 protein tyrosine phosphatase type IVA, member 16.5 5.19 1 rc_N80129_i_at 785 N80129 metallothionein 1L 12.6 3.54 rc_AA460914_at 380 AA460914 ESTs 7.4 4.58 rc_AA234996_s_at 147 AA234996 cytochrome C oxidase subunit VIa polypeptide 2 7.2 4.10 X66141_at 1078 X66141 myosin, light polypeptide 2, regulatory, cardiac, 6.6 3.80 slow AA234634_f_at 145 AA234634 CCAAT/enhancer binding protein (C/EBP), delta 6.2 4.35 rc_AA419011_at 296 AA419011 prostate androgen-regulated transcript 1 6.1 3.87 rc_N94303_at 797 N94303 ESTs 5.8 5.96 M20543_at 666 M20543 actin, alpha 1, skeletal muscle 5.5 3.20 rc_AA085943_s_at 58 AA085943 troponin T1, skeletal, slow 5.5 3.02 X06825_at 1050 X06825 tropomyosin 2 (beta) 5.2 3.35 AB000584_at 459 AB000584 prostate differentiation factor 5.1 3.80 M19309_s_at 665 M19309 troponin T1, skeletal, slow 5.0 3.41 rc_AA040433_at 24 AA040433 DKFZP586N2124 protein 5.0 2.62 rc_N32748_at 736 N32748 ESTs 5.0 3.36 rc_AA227926_at 135 AA227926 ESTs 4.8 5.39 rc_AA457566_at 375 AA457566 ESTs 4.7 4.22 rc_AA026641_s_at 16 AA026641 secretory leukocyte protease inhibitor 4.6 2.09 (antileukoproteinase) rc_AA053424_at 40 AA053424 serine/threonine protein kinase MASK 4.5 4.16 V00594_at 992 V00594 metallothionein 2A 4.5 3.71 rc_R16983_at 811 R16983 ESTs 4.5 3.23 U75272_s_at 984 U75272 progastricsin (pepsinogen C) 4.4 4.57 rc_T94447_s_at 928 T94447 cortic al thymocyte receptor (X. laevis CTX) like 4.4 3.50 U08021_at 942 U08021 nicotinamide N-**methyltransferase** 4.4 2.41 J03910_rna1_at 622 J03910 metallothionein 1G 4.3 2.79 rc_AA236545_at 156 AA236545 ESTs 4.2 2.41 rc_AA211443_at 127 AA211443 ESTs 4.2 4.49 rc_AA398908_at 251 AA398908 ESTs 4.2 2.64 X57129_at 1067 X57129 H1 histone family, member 2 4.2 3.88 M21665_s_at 670 M21665 myosin, heavy polypeptide 7, cardiac muscle, 4.1 3.61 beta X65614_at 1076 X65614 S100 calcium-binding protein P 4.1 4.03 rc_AA197112_r_at 119 AA197112 putative nuclear protein 4.1 3.07 M99487_at 716 M99487 folate hydrolase (prostate-specific membrane 4.0 2.65 antigen) 1 X04201_at 1045 X04201 neurotrophic tyrosine kinase, receptor, type 1 3.9 2.87 X05451_s_at 1046 X05451 ESTs 3.9 3.26 rc_AA435720_i_at 328 AA435720 tubulin, alpha 2 3.9 2.20 rc_N92502_s_at 794 N92502 ESTs 3.8 3.11 L77701_at 651 L77701 COX17 (yeast) homolog, cytochrome c oxidase 3.8 3.97 assembly protein HG2157-HT2227_at HG2157- ESTs 3.8 4.08 HT2227 X76717_at 1087 X76717 metallothionein 1L 3.8 5.82 HG1067-HT1067_r_at HG1067- ESTs 3.7 3.02 HT1067 rc_AA599331_at 433 AA599331 CGI-119 protein, uncharacterized bone marrow 3.6 4.90 protein BM039 M20642_s_at 667 M20642 ESTs 3.6 3.48 rc_AA055163_at 44 AA055163 calsequestrin 2, cardiac muscle 3.6 3.66 rc_AA127946_at 72 AA127946 DKFZP586B2022 protein 3.6 4.40 rc_AA022886_at 14 AA022886 retinal degeneration B beta 3.6 3.51 rc_AA342337_at 231 AA342337 ESTs 3.5 2.57 X02544_at 1042 X02544 orosomucoid 1 3.5 1.92 rc_T73433_s_at 912 T73433 angiotensinogen 3.5 3.10 M21494_at 669 M21494 creatine kinase, muscle 3.4 2.46 rc_AA488072_s_at 411 AA488072 cardiac ankyrin repeat protein 3.4 2.78 rc_AA293187_s_at 223 AA293187 B-cell CLL/lymphoma 3 3.4 1.62 rc_AA599522_r_at 437 AA599522 squamous cell carcinoma antigen recognised by 3.4 3.03 T cells rc_AA405488_at 268 AA405488 ESTs 3.4 2.57 rc_AA461453_at 382 AA461453 calcium binding protein Cab45 precursor, 3.4 3.10 rc_AA609006_at 440 AA609006 ESTs 3.4 2.30 rc_N24761_at 725 N24761 TU12B1-TY protein 3.4 3.89 rc_AA432162_at 324 AA432162 DKFZP586B2022 protein 3.4 2.78 X06256_at 1047 X06256 integrin, alpha 5 (fibronectin receptor, alpha 3.4 4.51 polypeptide) rc_AA045825_at 33 AA045825 ESTs 3.3 3.90 rc_AA478778_at 399 AA478778 ESTs 3.3

4.37 rc_N80129_f_at 785 N80129 metallothionein 1L 3.2 3.60 rc_AA182030_at 110 AA182030 pyruvate dehydrogenase kinase, isoenzyme 4 3.2 3.72 rc_AA102489_at 67 AA102489 hypothetical protein FLJ10337 3.2 2.20 rc_R46074_at 840 R46074 transforming, acidic coiled-coil containing protein 3.2 3.38 2 rc_AA599522_f_at 437 AA599522 squamous cell carcinoma antigen recognised by 3.2 2.36 T cells rc_AA165313_at 104 AA165313 ESTs 3.2 2.76 rc_AA429636_at 319 AA429636 hexokinase 2 3.2 3.12 rc_R71792_s_at 855 R71792 thrombospondin 1 3.1 2.31 U05861_at 940 U05861 aldo-keto reductase family 1, member C1 3.1 2.62 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase), aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3- alpha hydroxysteroid dehydrogenase, type III) rc_AA410311_at 275 AA410311 ESTs 3.1 3.52 rc_AA505136_at 426 AA505136 ESTs 3.1 3.00 rc_T68873_f_at 911 T68873 metallothionein 1L 3.0 3.18 X00371_ma1_at 1041 X00371 myoglobin 3.0 2.18 rc_AA099820_at 65 AA099820 ESTs 3.0 3.08 rc_T90190_s_at 925 T90190 H1 histone family, member 2 3.0 3.48 rc_AA227936_f_at 136 AA227936 parathymosin 3.0 1.76 X90568_at 1092 X90568 titin 3.0 2.83 rc_AA004699_at 1 AA004699 orphan G-protein coupled receptor 3.0 2.23 rc_F03969_at 528 F03969 ESTs 2.9 2.53 X93036_at 1093 X93036 FXYD domain-containing ion transport regulator 2.9 2.91 3 rc_R91484_at 863 R91484 ESTs 2.9 6.43 rc_AA025370_at 15 AA025370 K1AA0872 protein 2.9 2.87 X51441_s_at 1063 X51441 serum amyloid A1 2.9 1.78 X64177_f_at 1075 X64177 metallothionein 1H 2.9 3.36 rc_AA255480_at 173 AA255480 ECSIT 2.9 2.38 rc_AA476944_at 394 AA476944 ESTs 2.8 4.26 U78294_at 985 U78294 arachidonate 15-lipoxygenase, second type 2.8 1.82 rc_AA045487_at 31 AA045487 ESTs 2.8 2.75 rc_N74291_at 779 N74291 ESTs 2.8 1.88 rc_N91973_at 792 N91973 hypothetical protein,three prime repair 2.8 1.97 exonuclease 1 D81655_at 510 D81655 ESTs 2.8 1.89 U53225_at 971 U53225 sorting nexin 1 2.8 3.16 rc_H77597_f_at 594 H77597 metallothionein 1H 2.8 2.98 K02215_at 628 K02215 angiotensinogen 2.8 3.05 rc_AA464728_s_at 388 AA464728 ESTs 2.7 3.80 rc_W49708_at 1010 W49708 ESTs 2.7 3.52 rc_AA453435_at 364 AA453435 ESTs 2.7 4.78 rc_D11824_at 474 D11824 ESTs 2.7 3.70 rc_T56281_f_at 902 T56281 RNA helicase-related protein 2.7 2.62 rc_AA182882_at 111 AA182882 titin-cap (telethonin) 2.7 1.85 rc_AA447522_at 349 AA447522 ESTs 2.7 3.27 rc_N26904_at 731 N26904 FK506 binding protein precursor 2.7 3.21 rc_AA131919_at 75 AA131919 putative type II membrane protein 2.7 4.15 rc_R89840_at 862 R89840 ESTs 2.7 2.23 rc_W31470_at 998 W31470 thyroid hormone receptor-associated protein, 95-2.7 2.85 kD subunit rc_W92207_at 1036 W92207 ESTs 2.7 4.07 U96094_at 990 U96094 sarcolipin 2.7 2.23 rc_W70131_at 1024 W70131 ESTs 2.7 3.64 rc_AA435720_f_at 328 AA435720 tubulin, alpha 2 2.7 1.98 rc_AA284879_at 212 AA284879 ESTs 2.7 1.74 rc_H22453_at 564 H22453 ESTs 2.7 4.20 D14826_s_at 478 D14826 cAMP responsive element modulator 2.6 4.13 rc_N93798_at 796 N93798 protein tyrosine phosphatase type IVA, member 2.6 3.12 3 U41804_at 965 U41804 putative T1/ST2 receptor binding protein 2.6 4.37 rc_W20486_f_at 995 W20486 chromosome 21 open reading frame 56 2.6 2.74 rc_AA055768_at 45 AA055768 CGI-119 protein 2.6 2.13 rc_AA447977_s_at 352 AA447977 ESTs 2.6 3.22 AA380393_at 243 AA380393 SEC7 homolog 2.6 2.29 rc_N29568_at 732 N29568 thyroid hormone receptor-associated protein, 2.6 2.46 150 kDa subunit rc_AA426374_f_at 308 AA426374 tubulin, alpha 2 2.6 3.20 rc_H94471_at 604 H94471 occludin 2.6 2.19 rc_AA252219_at 169 AA252219 ESTs 2.6 3.83 rc_AA402000_at 259 AA402000 ESTs 2.6 2.29 rc_Z38744_at 1108 Z38744 putative gene product 2.6 4.18 AA045870_at 34 AA045870 ESTs 2.6 2.26 rc_R38678_at 823 R38678 ESTs 2.6 4.16 R39467_f_at 826 R39467 NEU1 protein 2.6 2.79 AA455001_s_at 368 AA455001 CGI-43 protein 2.6 5.34 rc_AA292328_at 221

AA292328 activating transcripti_n factor 5 2.6 2.88 X57348_s_at 1068 X57348 stratifin 2.6 2.48 rc_T95005_s_at 929 T95005 ESTs 2.5 3.30 AA410355_at 276 AA410355 ribosomal protein S6 kinase, 70 kD, polypeptide 2.5 2.31 AA036900_at 21 AA036900 ESTs 2.5 2.45 rc_F02204_at 521 F02204 BAI1-associated protein 2 2.5 2.26 U26173_s_at 958 U26173 nuclear factor, interleukin 3 regulated 2.5 3.91 rc_AA477767_at 396 AA477767 ESTs 2.5 3.17 rc_AA504805_s_at 424 AA504805 interferon stimulated gene (20 kD) 2.5 3.79 rc_R33627_i_at 818 R33627 ESTs 2.5 1.99 rc_T40995_f_at

PGPUB-DOCUMENT-NUMBER: 20030118599

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030118599 A1

TITLE: Compositions and methods for the therapy and diagnosis of lung cancer

PUBLICATION-DATE: June 26, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Algate, Paul A.	Issaquah	WA	US	
Lodes, Michael J.	Seattle	WA	US	
Wang, Tongtong	Medina	WA	US	
Fan, Liqun	Bellevue	WA	US	
McNeill, Patricia D.	Federal Way	WA	US	

APPL-NO: 10/ 144649

DATE FILED: May 10, 2002

RELATED-US-APPL-DATA:

child 10144649 A1 20020510

parent continuation-in-part-of 09854133 20010511 US PENDING

child 09854133 20010511 US

parent continuation-in-part-of 09738973 20001214 US PENDING

child 09738973 20001214 US

parent continuation-in-part-of 09704512 20001101 US PENDING

child 09704512 20001101 US

parent continuation-in-part-of 09667170 20000920 US PENDING

child 09667170 20000920 US

parent continuation-in-part-of 09640878 20000818 US ABANDONED

child 09640878 20000818 US

parent continuation-in-part-of 09588937 20000605 US ABANDONED

child 09588937 20000605 US

parent continuation-in-part-of 09538037 20000329 US ABANDONED

child 09538037 20000329 US

parent continuation-in-part-of 09518809 20000303 US ABANDONED

child 09518809 20000303 US

parent continuation-in-part-of 09476235 19991230 US ABANDONED

child 09476235 19991230 US

parent continuation-in-part-of 09370838 19990809 US GRANTED

parent-patent 6444425 US

child 09370838 19990809 US

parent continuation-in-part-of 09285323 19990402 US ABANDONED

US-CL-CURRENT: 424/185.1, 435/183 , 435/320.1 , 435/325 , 435/6 , 435/69.1 , 435/7.23 , 536/23.2

ABSTRACT:

Compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compositions comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is related to U.S. patent application Ser. No. 09/854,133, filed May 11, 2001; U.S. patent application Ser. No. 09/738,973, filed Dec. 14, 2000; U.S. patent application Ser. No. 09/704,512, filed Nov. 1, 2000; U.S. patent application Ser. No. 09/667,170, filed Sep. 20, 2000; U.S. Provisional Application No. 60/229,763, filed Sep. 1, 2000; U.S. patent application Ser. No. 09/640,878, filed Aug. 18, 2000; U.S. patent application Ser. No. 09/588,937, filed Jun. 5, 2000; U.S. patent application Ser. No. 09/538,037, filed Mar. 29, 2000; U.S. patent application Ser. No. 09/518,809, filed Mar. 3, 2000; U.S. patent application Ser. No. 09/476,235 filed Dec. 30, 1999; U.S. patent application Ser. No. 09/370,838, filed Aug. 9, 1999; and U.S. patent application Ser. No. 09/285,323, filed Apr. 2, 1999, each a CIP of the previous application and all pending, and incorporated herein by reference.

---------- KWIC ---------

Detail Description Table CWU - DETL (3):

4TABLE 4 GenBank Clone SEQ ID NO: Accession Description 55163 458, 459 Novel in Genbank 55158 452 Novel in Genbank Homology to known sequences with unknown function 55153 443, 444 7018516 H. sapiens mRNA; cDNA DKFZp434M035 55154 445, 446 6437562 H. sapiens Chr 22q11 PAC Clone p393 55157 450, 451 2887408 H. sapiens KIAA0417 mRNA 55165 462, 463 3970871 H. sapiens HRIHFB2122 mRNA Homology to known sequences with known function 55155 447 7677405 H. sapiens F-box protein FBS (FBS) 55156 448, 449 3929584 H. sapiens EEN pseudogene 55161 454, 455 4503350 H. sapiens DNA (cytosine-5-)-**methyltransferase** 1 (DNMT1) 55162 456, 457 31220 ERK1 mRNA for protein serine/threonine kinase 55164 460, 461 6677666 H. sapiens RNA-binding protein (autoantigenic) (RALY) 55166 464, 465 3249540 H. sapiens ribonuclease P protein subunit p40 (RPP40) 55167 466, 467 7657497 H. sapiens renal tumor antigen (RAGE) 55168 468, 469 2873376 H. sapiens exportin t mRNA 55169 470, 471 3135472 H. sapiens Cre binding protein-like 2 mRNA 55171 474 4759151 H. sapiens spermine synthase (SMS) 55173 476 6688148 H. sapiens partial mRNA for NICE-3 protein 55174 477, 478 531394 Human **transcriptional coactivator** PC4 55175 479 6563201 H. sapiens translation initiation factor eIF-2b delta subunit 55176 480 29860 hCENP-Bgene, for centromere autoantigen B (CENP-B) Homology to Ribosomal Protein 55159 453 337494 Ribosomal protein L7a (surf 3) large subunit mRNA 55170 472, 473 4506648 H. sapiens mRNA for ribosomal protein L3 55172 475 388031 H. sapiens ribosomal protein L11

PGPUB-DOCUMENT-NUMBER: 20030114402

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030114402 A1

TITLE: Modulators of DNA cytosine-5 methyltransferase and methods for use thereof

PUBLICATION-DATE: June 19, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Reich, Norbert O.	Santa Barbara	CA	US	
Flynn, James	Goleta	CA	US	

APPL-NO: 10/ 010476

DATE FILED: December 7, 2001

RELATED-US-APPL-DATA:

child 10010476 A1 20011207

parent division-of 09485071 20000203 US PENDING

non-provisional-of-provisional 60057411 19970829 US

US-CL-CURRENT: 514/44, 536/23.1

ABSTRACT:

A synthetic oligonucleotide comprising a C-5 methylcytosine and which recognizes and binds an allosteric site on DNA methyltransferase thereby inhibiting DNA methyltransferase activity is disclosed. Also disclosed is a composition comprising a synthetic oligonucleotide of the invention. The composition is useful for inhibiting DNA methyltransferase activity, thereby inhibiting the methylation of DNA. The composition can be a pharmaceutical composition useful for treating disorders associated with methylation defects, such as cancer and certain developmental disorders. Also disclosed is a method of inhibiting methylation of DNA. The method involves contacting a DCMTase with a synthetic oligonucleotide of the invention in the presence of the DNA, thereby resulting in an enzyme/synthetic oligonucleotide complex. The presence of the complex prevents catalysis, thereby inhibiting DNA methyltransferase activity. Also disclosed is a method of treating a disorder of cell proliferation or development by administering to a subject a synthetic oligonucleotide of the invention. The inhibition of DNA methyltransferase prevents the methylation of DNA thereby treating the disorder of cell proliferation or development.

[0001] This application is based on U.S. provisional patent application serial

No. 60/057,411, filed Aug. 29, 1997, the entire contents of which are hereby incorporated by reference into this application. Throughout this application various publications are referenced. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

---------- KWIC ---------

Detail Description Paragraph - DETX (173):

[0214] Regulation of DNA replication and **transcriptional activation** by single-stranded DNA is known to occur (Takai, T., et al., 1994, Molecular cloning of MSSP-2, a c-myc gene single-strand binding protein: characterization of binding specificity and DNA replication activity, Nucleic Acids Res. 22:55776-5581; Rajavashisth, T. B., et al., 1989, Identification of a zinc finger protein that binds to the sterol regulatory element, Science 245:640-643; Tomonaga, T., & Levens, D., 1996, **Activating transcription** from single stranded DNA, Proc. Natl. Acad. Sci. USA 93:5830-5835). Nucleic acid regulation of DCMTase activity has previously been demonstrated. However, the requirement for micromolar concentrations of the polynucleic acids studied by Bolden et al. (1984, DNA methylation. Inhibition of de novo and maintenance methylation in vitro by RNA an dsynthetic polynucleotides, J. Biol. Chem 259:12437-12443) to inhibit DCMTase implicates poor binding to the same site suggested in our studies with GC-box b.sup.MET, or direct binding at the active site as competitive inhibitors. A stimulatory, cis-regulation by methylated CpG sites was reported to occur within single-stranded DNA using crude extracts (Christman, J. K., et al., 1995, 5-Methyl-2'-deoxycytidine in single-stranded DNA can act in cis to signal de novo DNA methylation, Proc. Natl. Acad. Sci. USA 92:7347-7351). While the mechanisms of regulation remain obscure in these cases, it is clear that they are distinct from the inhibition described herein. As previously stated, synthetic peptides mimicking portions of the DCMTase amino-terminus have been shown to gel mobility shift double-stranded DNA (Chuang, L. S., et al., 1996, Characterisation of independent DNA and multiple Zn-binding domains at the N terminus of human DNA-(cytosine-5) **methyltransferase**: modulating the property of a DNA-binding domain by contiguous Zn-binding motifs, Chia, J., and Li, B. F. L, J. Mol. Biol. 257:935-948). Although single-stranded DNA was apparently not studied, it would be interesting to systematically test these polypeptides for single-stranded DNA binding with and without methylated CpG dinucleotides.

PGPUB-DOCUMENT-NUMBER: 20030105593

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030105593 A1

TITLE: Selection of sites for targeting by zinc finger proteins and methods of designing zinc finger proteins to bind to preselected sites

PUBLICATION-DATE: June 5, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Eisenberg, Stephen P.	Boulder	CO	US	
Case, Casey C.	San Mateo	CA	US	
Cox, George N. III	Louisville	CO	US	
Jamieson, Andrew	San Francisco	CA	US	
Rebar, Edward J.	Berkeley	CA	US	

APPL-NO: 10/ 113424

DATE FILED: March 28, 2002

RELATED-US-APPL-DATA:

child 10113424 A1 20020328

parent division-of 09229007 19990112 US ABANDONED

US-CL-CURRENT: 702/19, 435/226

ABSTRACT:

The invention provides criteria and methods for selecting optimum subsequence(s) from a target gene for targeting by a zinc finger protein. Some of the methods of target site selection seek to identify one or more target segments having a DNA motif containing one or more so-called D-able subsites having the sequence 5'NNGK3'. Other methods of the invention are directed to selection of target segments within target genes using a correspondence regime between different triplets of three bases and the three possible positions of a triplet within a nine-base site. In another aspect, the invention provides methods of designing zinc finger proteins that bind to a preselected target site. These methods can be used following the preselection of target sites according to the procedures and criteria described above. The methods of design use a database containing information about previously characterized zinc finger proteins.

---------- KWIC ---------

Detail Description Paragraph - DETX (42):

[0070] Zinc finger proteins are often expressed with a heterologous domain as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcripti n factor domains (activat rs,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bel, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for represssing expression of a target gene is a the KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J. Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell. Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J. Virol. 72:5610-5618 (1998) and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

PGPUB-DOCUMENT-NUMBER: 20030104526

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030104526 A1

TITLE: Position dependent recognition of GNN nucleotide triplets by zinc fingers

PUBLICATION-DATE: June 5, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Liu, Qiang	Foster City	CA	US	

APPL-NO: 09/ 989994

DATE FILED: November 20, 2001

RELATED-US-APPL-DATA:

child 09989994 A1 20011120

parent continuation-in-part-of 09535008 20000323 US GRANTED

parent-patent 6465629 US

child 09989994 A1 20011120

parent continuation-in-part-of 09716637 20001120 US PENDING

non-provisional-of-provisional 60126238 19990324 US

non-provisional-of-provisional 60126239 19990324 US

non-provisional-of-provisional 60146595 19990730 US

non-provisional-of-provisional 60146615 19990730 US

US-CL-CURRENT: 435/69.1, 435/226 , 435/320.1 , 435/325 , 435/6 , 536/23.2

ABSTRACT:

The specificity of binding of a zinc finger to a triplet or quadruplet nucleotide target subsite depends upon the location of the zinc finger in a multifinger protein and, hence, upon the location of its target subsite within a larger target sequence. The present disclosure provides zinc finger amino acid sequences for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite, that have been optimized with respect to the location of the subsite within the target site. Accordingly, the disclosure provides finger position-specific amino acid sequences for the

recognition of GNN target subsites. This allows the construction of multi-finger zinc finger proteins with improved affinity and specificity for their target sequences, as well as enhanced biological activity.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] The present application is a continuation-in-part of copending U.S. patent application Ser. No. 09/535,008, filed Mar. 23, 2000, which application claims the benefit of U.S. provisional applications No. 60/126,238, filed Mar. 24, 1999, No. 60/126,239 filed Mar. 24, 1999, No. 60/146,595 filed Jul. 30, 1999 and No. 60/146,615 filed Jul. 30, 1999. The present application is also a continuation-in-part of copending U.S. patent application Ser. No. 09/716,637, filed Nov. 20, 2000. The disclosures of all of the aforementioned applications are hereby incorporated by reference in their entireties for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (44):

[0067] Zinc finger proteins are often expressed with a heterologous domain as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcription factor domains (activators,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for represssing expression of a target gene is a KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J. Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell. Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J. Virol. 72:5610-5618 (1998)and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

PGPUB-DOCUMENT-NUMBER: 20030095960

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030095960 A1

TITLE: Human transferases

PUBLICATION-DATE: May 22, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 284985

DATE FILED: October 29, 2002

RELATED-US-APPL-DATA:

child 10284985 A1 20021029

parent division-of 09490032 20000121 US GRANTED

parent-patent 6471959 US

child 09490032 20000121 US

parent division-of 09109204 19980630 US GRANTED

parent-patent 6060250 US

US-CL-CURRENT: 424/94.5, 435/193 , 435/252.3 , 435/320.1 , 435/325 , 435/6 , 435/69.1 , 536/23.2 , 800/8

ABSTRACT:

The invention provides three human transferases (HUTRAN) and polynucleotides which identify and encode HUTRAN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating or preventing disorders associated with expression of HUTRAN.

[0001] This application is a divisional application of U.S. application Ser. No. 09/490,032, filed Jan. 21, 2000, which is a divisional application of U.S.

application Ser. No. 09/109,204, filed Jun. 30, 1998, now U.S. Pat. No. 6,060,250, issued May 9, 2000, all of which are entitled HUMAN TRANSFERASES, and all of which are expressly incorporated herein by reference.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (7):

[0006] Protein-**arginine methyltransferases** catalyze the posttranslational methylation of arginine residues in proteins, resulting in the mono- and dimethylation of arginine on the guanidino group. Known substrates are histones, heterogeneous nuclear ribonucleoproteins (hnRNPs), and myelin basic protein. This otherwise unusual posttranslational modification is common in hnRNPs and may regulate their function. hnRNPs function in the nucleus in mRNA processing, splicing, and transport into the cytoplasm. Homologous protein-**arginine methyltransferases** that methylate hnRNPs have been cloned from yeast, rat, and man. These protein-**arginine methyltransferases** contain five sequence motifs, termed region I, post-region I, region II, region III, and post-region III, that may be involved in binding S-adenosyl-methionine. One human gene (HRMT1L1) encodes a 433 amino acid protein. The other human gene (HRMT1L2) may be alternatively spliced to yield three protein-**arginine methyltransferases,** of length 343, 347, and 361 amino acids respectively, with different amino termini. The protein encoded by the cloned rat protein-**arginine methyltransferase** gene (PRMT1) interacts with the TIS21 protein and the homologous BTG1 protein. The intermediate-early TIS21 protein is the product of a gene induced by treatment of cells with mitogens such as epidermal growth factor, and the BTG1 protein is the product of a human gene located near a chromosome translocation breakpoint associated with chronic lymphocytic leukemia. The HRMT1L2 protein interacts with the cytoplasmic domain of the interferon receptor. This interaction suggests that protein methylation may be an important signaling mechanism for cytokine receptors. (Lin, W. -J. et al. (1996) J. Biol. Chem. 271:15034-15044; Abramovich, C. et al. (1997) EMBO J. 16:260-266; and Scott, H. S. et al. (1998) Genomics 48:330-340.)

Brief Description of Drawings Paragraph - DRTX (4):

[0023] FIGS. 3A, 3B, and 3C show the amino acid sequence alignment between HUTRAN-3 (2525071; SEQ ID NO:3) and human **arginine methyltransferase** (GI 1808648; SEQ ID NO:32).

Detail Description Paragraph - DETX (53):

[0075] As shown in Table 2, each HUTRAN has been characterized with regard to its chemical and structural similarity with transferase molecules. As shown in FIGS. 1A and 1B, HUTRAN-1 and human glutamine-phenylpyruvate aminotransferase (GI 758591; SEQ ID NO:30) share 49% identity. As shown in FIGS. 2A and 2B, HUTRAN-2 and rat kynurenine/.alpha.-aminoadipate aminotransferase (GI 1050752; SEQ ID NO:31) share 71% identity. As shown in FIGS. 3A, 3B, and 3C, HUTRAN-3 and human **arginine methyltransferase** (GI 1808648; SEQ ID NO:32) share 27% identity.

Detail Description Paragraph - DETX (91):

[0113] Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between HUTRAN-1 and glutamine-phenylpyruvat- e aminotransferase from man (GI 758591), between HUTRAN-2 and kynurenine/.alpha.-aminoadipate aminotransferase from rat (GI 1050752), and between HUTRAN-3 and **arginine methyltransferase** from man (GI 1808648). In addition, HUTRAN is expressed in cancerous, inflamed, male and female reproductive, nervous, and gastrointestinal tissues. Therefore, HUTRAN appears to play a role in autoimmune/inflammatory, neurological, reproductive, and gastrointestinal disorders, and cancer.

PGPUB-DOCUMENT-NUMBER: 20030092095

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030092095 A1

TITLE: Screening, diagnostic and therapeutic methods relating to RIZ

PUBLICATION-DATE: May 15, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Huang, Shi	San Diego	CA	US	

APPL-NO: 10/ 142650

DATE FILED: May 9, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60290481 20010511 US

US-CL-CURRENT: 435/15

ABSTRACT:

The invention provides a method of screening for a compound that modulates RIZ histone methyltransferase (HMT) activity, by contacting a RIZ or RIZ fragment having HMT activity with one or more candidate compounds, and determining histone methyltransferase activity of the contacted RIZ or RIZ fragment. Also provided is a method of screening for a compound that modulates progesterone receptor (PR) activity, by providing a RIZ1 modulatory compound, and determining the ability of the RIZ1 modulatory compound to modulate PR activity. Further provided is a method of identifying an individual with an estrogen receptor positive (ER+) tumor having a reduced likelihood of responding to endocrine therapy. The method involves determining the RIZ1 status of the tumor, wherein an abnormal RIZ1 status identifies the individual as an individual with a reduced likelihood of responding to endocrine therapy.

[0001] This application claims the benefit of U.S. Provisional Application Serial No. 60/290,481, filed May 11, 2001, which is incorporated herein by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (53):

[0079] RIZ1 functional activities are described herein or are known in the art. Exemplary activities include, for example, **transcriptional activati n**

(see, for example, U.S. Pat. No. 5,811,304), transcriptional repression (see, for example, Xie et al., J. Biol. Chem. 272:26360-26366 (1997)), histone **methyltransferase** activity (see Example I) and hormone receptor coactivation (see Examples I and II).

Detail Description Paragraph - DETX (54):

[0080] Suitable assays for identifying compounds that modulate RIZ1 **transcriptional activation,** repression and coactivation function can be determined by the skilled person. Such assays are generally based on co-expression of RIZ1 and an appropriate promoter-linked reporter gene in a cell, under conditions where a certain amount of transcription occurs, contacting the cell with the candidate compound, and determining whether there is a change (i.e. either an increase or decrease) in transcriptional activity. Transcription based assays are well known in the art, and readily amenable to high-throughput screening assays. **Methyltransferase** activity assays have been described above.

PGPUB-DOCUMENT-NUMBER: 20030092000

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030092000 A1

TITLE: Selection of sites for targeting by zinc finger proteins and methods of designing zinc finger proteins to bind to preselected sites

PUBLICATION-DATE: May 15, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 825242

DATE FILED: April 2, 2001

RELATED-US-APPL-DATA:

child 09825242 A1 20010402

parent division-of 09229007 19990112 US ABANDONED

US-CL-CURRENT: 435/6, 702/20

ABSTRACT:

The invention provides criteria and methods for selecting optimum subsequence(s) from a target gene for targeting by a zinc finger protein. Some of the methods of target site selection seek to identify one or more target segments having a DNA motif containing one or more so-called D-able subsites having the sequence 5'NNGK3'. Other methods of the invention are directed to selection of target segments within target genes using a correspondence regime between different triplets of three bases and the three possible positions of a triplet within a nine-base site. In another aspect, the invention provides methods of designing zinc finger proteins that bind to a preselected target site. These methods can be used following the preselection of target sites according to the procedures and criteria described above. The methods of design use a database containing information about previously characterized zinc finger proteins.

---------- KWIC ---------

Detail Description Paragraph - DETX (35):

[0065] Zinc finger proteins are often expressed with a heterologous domain as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcription factor domains (activators,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for represssing expression of a target gene is a the KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J. Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell. Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J. Virol. 72:5610-5618 (1998)and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

PGPUB-DOCUMENT-NUMBER: 20030088061

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030088061 A1

TITLE: Materials and methods to modulate ligand binding/enzymatic activity of alpha/beta proteins containing an allosteric regulatory site

PUBLICATION-DATE: May 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 976935

DATE FILED: October 12, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60239750 20001012 US

US-CL-CURRENT: 530/350

ABSTRACT:

Methods of modulating binding between an .alpha./.beta. protein and a binding partner are provided, along with methods of identifying modulators and their use.

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Application Serial No. 60/239,750, filed Oct. 12, 2000.

---------- KWIC ---------

Summary of Invention - Table CWU - BSTL (7):

7. Methylated DNA-protein cysteine methyltransferase domain (1) 1. Methylated DNA-protein cysteine methyltransferase domain (3) 56. Phosphorylase/hydrolase-like (6) core: 3 layers, a/b/a; mixed sheet of 5 strands: order 21354: strand 4 is antiparallel to the rest; contains crossover loops 1. Hydrogenase maturating endopeptidase HybD (1) the fold coincides with the consensus core structure 1. Hydrogenase maturating endopeptidase HybD (1) 2. Purine and uridine phosphorylases (1) complex architecture; contains mixed beta-sheet of 8 strands, order 23415867, strands 3, 6 & 7 are antiparallel to the rest; and barrel, closed; n = 5, S = 8 1.

Purine and uridine phosphorylases (6) 3. Peptidyl-tRNA hydrolase (1) 1. Peptidyl-tRNA hydrolase (1) 4. Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) (1) 1. Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) (2) 5. Zn-dependent exopeptidases (5) core: mixed beta-sheet of 8 strands, order 12435867; strands 2, 6 & 7 are antiparallel to the rest 1. Pancreatic carboxypeptidases (6) 2. Carboxypeptidase T (1) 3. Leucine aminopeptidase, C-terminal domain (1) 4. Bacterial exopeptidases (3) 5. Transferrin receptor ectodomain, protease-like domain (1) 6. LigB subunit of an aromatic-ring-opening dioxygenase LigAB (1) circular permutation of the common fold, most similar to the PNP fold 1. LigB subunit of an aromatic-ring-opening dioxygenase LigAB (1) 57. Molybdenumm cofactor biosynthesis protein MogA (1) 3 layers: a/b/a; mixed beta-sheet of 5 strands; order: 21354, strand 5 is antiparallel to the rest; permutation of the Phosphorylase/hydrolase-like fold 1. Molybdenumm cofactor biosynthesis protein MogA (1) 1. Molybdenumm cofactor biosynthesis protein MogA (1) 58. Amino acid dehydrogenase-like, N-terminal domain (1) 3 layers: a/b/a; mixed beta-sheet of 5 strands; 12435, strand 2 is antiparallel to the rest 1. Amino acid dehydrogenase-like, N-terminal domain (3) 1. Amino acid dehydrogenases (7) dimerisation domain 2. Tetrahydrofolate dehydrogenase/cyclohydrolase (3) 3. Mitochondrial NAD(P)-dependent malic enzyme (1) this domain is decorated with additional structures; includes N-terminal additional subdomains 59. Glutamate ligase domain (1) 3 layers: a/b/a; mixed beta-sheet of 6 strands, order 126345, strand 1 is antiparallel to the rest 1. Glutamate ligase domain (2) 1. MurD/MurF C-terminal domain (2) 2. Folylpolyglutamate synthetase, C-terminal domain (1) 60. Phosphoglycerate mutase-like (1) core: 3 layers, a/b/a; mixed beta-sheet of 6 strands, order 324156; strand 5 is antiparallel to the rest 1. Phosphoglycerate mutase-like (4) 1. Phosphoglycerate mutase (1) 2. Acid phosphatase (2) 3. Phytase (myo-inositol-hexakispho- sphate-3-phosphohydrolase) (3) 4. 6-phosphofructo-2-kinase/fructos- e-2,6-bisphosphatase, phosphatase domain (1) 61. PRTase-like (1) core: 3 layers, a/b/a; mixed beta-sheet of 6 strands, order 321456; strand 3 is antiparallel to the rest 1. PRTase-like (2) 1. Phosphoribosyltransferases (PRTases) (14) 2. Phosphoribosylpyrophosphate synthetase (1) duplication: consists of two domains of this fold 62. Integrin A (or I) domain (1) core: 3 layers, a/b/a; mixed beta-sheet of 6 strands, order 321456: strand 3 is antiparallel to the rest 1. Integrin A (or I) domain (1) 1. Integrin A (or I) domain (7) 63. Glutaconate-CoA transferase subunits (1) core. 3 layers: a/b/a; parallel or mixed b-sheet of 6 strands, order 432156; part of sheet is folded upon itself and forms a barrel-like structure 1. Glutaconate-CoA transferase subunits (1) 1. Glutaconate-CoA transferase subunits (2) 64. Pyruvate-ferredoxin oxidoreductase, PFOR, domain III (1) 3 layers. a/b/a, mixed beta-sheet of 6 strands, order 231456; strand 3 is antiparallel to the rest 1. Pyruvate-ferredoxin oxidoreductase, PFOR, domain III (1) 1. Pyruvate-ferredoxin oxidoreductase, PFOR, domain III (1) 65. Formyltransferase (1) 3 layers: a/b/a; mixed beta-sheet of 7 strands, order 3214567; strand 6 is antiparallel to the rest 1. Formyltransferase (1) 1. Formyltransferase (2) 66. S-adenosyl-L-methionine-dependent methyltransferases (1) core: 3 layers, a/b/a; mixed beta-sheet of 7 strands, order 32145 76, strand 7 is antiparallel to the rest 1. S-adenosyl-L-methionine-dependent methyltransferases (11) 1. Catechol O-methyltransferase, COMT (1) 2. RNA methyltransferase FtsJ (1) 3. Fibrillarin homologue (1) 4. Hypothetical protein MJ0882 (1) 5. Glycine

N-methyltransferase (1) 6. **Arginine methyltransferase,** HMT 1 (1) lacks the last two strands of the common fold replaced with a beta-sandwich oligomerisation subdomain 7. Protein-L-isoaspartate O-methyltransferase (1) another C-terminal variation of the common fold with additional alpha + beta subdomain 8. Chemotaxis receptor methyltransferase CheR, C-terminal domain (1) contains additional N-terminal all-alpha domain, res. 11-91 9. RNA methylases (3) 10. DNA methylases (5) 11. Type II DNA methylase (2) circularly permuted version of the common fold 67. PLP-dependent transferases (1) main domain: 3 layers: a/b/a, mixed beta-sheet of 7 strands, order 3245671; strand 7 is antiparallel to the rest 1. PLP-dependent transferases (5) 1. AAT-like (9) 2. Beta-eliminating lyases (2) 3. Cystathionine synthase-like (8) 4. omega-Amino acid:pyruvate aminotransferase-like (15) 5. Ornithine decarboxylase major domain (1) 68. Nucleotide-diphospho-sugar transferases (1) 3 layers: a/b/a; mixed beta-sheet of 7 strands, order 3214657; strand 6 is antiparallel to the rest 1. Nucleotide-diphospho-sugar transferases (8) 1. Spore coat polysaccharide biosynthesis protein SpsA (1) 2. beta 1,4 galactosyltransferase (b4GalTI) (1) 3. CMP acylneuraminate synthetase (1) 4. Galactosyltransferase LgtC (1) 5 N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain (1) 6. glucose-1-phosphate thymidylyltransferase RmlA (1) 7. 1,3-Glucuronyltransferase I (glcAT-I) (1) 8. Molybdenum cofactor biosynthesis protein MobA (1) 69. alpha/beta-Hydrolases (1) core: 3 layers, a/b/a; mixed beta-sheet of 8 strands, order 12435678, strand 2 is antiparallel to the rest 1. alpha/beta-Hydrolases (20) many members have left-handed crossover connection between strand 8 and additional strand 9 1. Acetylcholinesterase-like (8) 2. Carboxylesterase (2) 3. Mycobacterial antigens (2) 4. Prolyl oligopeptidase, C-terminal domain (1) 5. Serine carboxypeptidase (4) 6. Gastric lipase (1) 7. Proline iminopeptidase (2) 8. Haloalkane dehalogenase (3) 9. Dienelactone hydrolase (2) 10. Carbon-carbon bond hydrolase (1) 11. Epoxide hydrolase (3) 12. Haloperoxidase (5) 13. Thioesterases (2) 14. Carboxylesterase/thioesterase 1 (2) 15. A novel bacterial esterase (1) 16. Lipase (1) 17. Fungal lipases (9) 18. Bacterial lipase (5) 19. Pancreatic lipase, N-terminal domain (6) 20. Hydroxynitrile lyase (2) 70. Nucleoside hydrolase (1) core: 3 layers, a/b/a; mixed beta-sheet of 8 strands, order 32145687; strand 7 is antiparallel to the rest 1. Nucleosidehydrolase (1) 1. Nucleoside hydrolase (2) 71. Dihydrofolate reductases (1) 3 layers: a/b/a; mixed beta-sheet of 8 strands, order 34251687; strand 8 is antiparallel to the rest 1. Dihydrofolate reductases (1) 1. Dihydrofolate reductases (10) 72. Ribokinase-like (2) core: 3 layers: a/b/a; mixed beta-sheet of 8 strands, order 21345678, strand 7 is antiparallel to the rest

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PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030087817 A1

TITLE: Regulation of endogenous gene expression in cells using zinc finger proteins

PUBLICATION-DATE: May 8, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 897844

DATE FILED: July 2, 2001

RELATED-US-APPL-DATA:

child 09897844 A1 20010702

parent continuation-of 09229037 19990112 US PENDING

US-CL-CURRENT: 514/12, 435/455

ABSTRACT:

The present invention provides methods for modulating expression of endogenous cellular genes using recombinant zinc finger proteins.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is related to Townsend and Townsend and Crew docket number 019496-001800, U.S. Ser. No. _____, filed Jan. 12, 1999, herein incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (29):

[0075] A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B

subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (90):

[0136] Common regulatory domains for addition to the ZFP include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20030082819

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030082819 A1

TITLE: Methods of detecting protein **arginine methyltransferase,** and uses related thereto

PUBLICATION-DATE: May 1, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 152158

DATE FILED: May 20, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60292075 20010518 US

US-CL-CURRENT: 436/86, 436/171 , 436/173

ABSTRACT:

This invention relates to methods and reagents for detecting the presence of symmetrically and asymmetrically methylated arginine residues, either along or in polypeptides, using mass spectrometry. It also provides methods of determining structures of methylated arginine residues, methods of identifying substrates of PMRTs, and methods of conducting proteomic business using any of the suitable methods recited above.

REFERENCE TO RELATED APPLICATION

[0001] This Application claims priority to U.S. Provisional Application 60/292,075, filed on May 18, 2001, the entire content of which is hereby incorporated by reference.

---------- KWIC ---------

Title - TTL (1):
Methods of detecting protein **arginine methyltransferase,** and uses related thereto

Summary of Invention Paragraph - BSTX (2):

[0002] Post-translational modifications can have profound effects on the activities of proteins. One type of protein modification involves the transfer of methyl groups to a specific arginine residue resulting in the formation of dimethylarginine. This reaction is catalyzed by a protein **arginine methyltransferase** (PRMT). PRMTs have been implicated in a variety of processes, including cell proliferation, signal transduction, and protein trafficking. Arginine dimethylation has been implicated in such cellular processes as transcription (Chen et al. 1999 Science 284:2174-7), signal transduction (Bedford et al. 2000 J Biol Chem 275:16030-6; Mowen et al. 2001 Cell 104:731-41), nuclear export (Shen et al. 1998 Genes Dev. 12:679-91), myelin integrity (Kim et al. 1997 Int J Biochem Cell Biol 29:743-51) and possibly antigenicity (Brahms et al. 2000 J Biol Chem 275:17122-9).

Summary of Invention Paragraph - BSTX (4):

[0004] Most substrates for type I enzymes bind nucleic acid, usually RNA. These include heterogeneous nuclear RNA binding proteins (hnRNPs), which collectively contain 65% of the nuclear asymmetric dimethylarginine, as well as fibrillarin and nucleolin (Lischwe et al. 1985 J. Biol. Chem. 260:14304-14310; Liu et al. 1995 Mol. Cell. Biol. 15:2800-2808; Najbauer et al. 1993 J. Biol. Chem. 268:10501-10509). Examples of physiological substrate of symmetric (type II) **arginine methyltransferase** include myelin basic protein, a major protein component of the myelin sheath, as well as the Sm proteins D1 and D3, which are components of small nuclear ribonucleoproteins.

Summary of Invention Paragraph - BSTX (7):

[0007] Interactions between the PRMT1 enzyme and potential signaling components have also emerged from yeast two-hybrid screens. The immediate-early gene product TIS21 (BTG2) and the leukemia-associated gene product BTG1 interact with PRMT1 and can modulate its enzymatic activity in vitro. TIS21 and BTG1 both belong to a family of mitogen-induced proteins implicated in negative regulation of the cell cycle. PRMT1 also binds to the cytoplasmic domain of the IFNAR1 chain of the alpha beta interferon receptor, while growth-inhibitory effects of interferon were suppressed by antisense oligonucleotides directed against the methyltransferase. Finally, a novel **arginine methyltransferase** (CARM1) associates with p160 coactivators and serves as a secondary coactivator of nuclear hormone receptors.

Summary of Invention Paragraph - BSTX (10):

[0010] Efforts to understand the biochemical function of mammalian **arginine methyltransferases** are complicated by several factors, including the existence of multiple enzymes and the fact that methyltransferase inhibitors nonspecifically target multiple processes in which S-adenosylmethionine serves as a methyl donor. In yeast, functional studies of arginine methylation have benefited greatly from genetic approaches that have led to the isolation of cells deficient in the enzyme. In principle, gene targeting strategies could be used for similar studies of the mammalian enzymes, assuming that the proteins are not required for cell viability.

Summary of Invention Paragraph - BSTX (15):

[0014] Still another aspect of the invention provides a method for identifying substrates of a protein **arginine methyltransferase**. According to the subject embodiment, mass spectra are obtained for one or more sample polypeptides which have been exposed to a protein **arginine methyltransferase** (PRMT) under conditions wherein methylation, if any, of arginine residues in a substrate protein of the PRMT can occur. The presence of dimethylarginine residues in the sample polypeptide can be identified by the presence of mass modified arginine (relative to unmodified arginine) in the mass spectra of the sample protein. To ascertain the nature of the methylation of a dimethylarginine residue, further determines if a neutral loss spectra of the sample peptide shows one or both of neutral loss of monomethylamine, dimethylcarbodiimide, and/or neutral loss of dimethylamine. Neutral loss of monomethylamine and of dimethylcarbodiimide indicates the presence of a symmetrically dimethylated arginine residue whereas neutral loss of dimethylamine indicates the presence of a asymmetrically dimethylated arginine residue. In certain preferred embodiments, the sequence of at least that portion of a polypeptide including a dimethylarginine residue is determined, e.g., based on the mass spectra of the polypeptide. The subject method can be carried out for a library of sample polypeptides.

Summary of Invention Paragraph - BSTX (16):

[0015] Thus, the invention provides A method for identifying substrates of a protein **arginine methyltransferase** comprising: (i) obtaining mass spectra for one or more sample polypeptides which have been exposed to a protein **arginine methyltransferase** (PRMT) under conditions wherein methylation, if any, of arginine residues in a substrate protein of the PRMT can occur; (ii) identifying the presence of dimethylarginine residues in the sample polypeptide by the presence of mass modified arginine in the mass spectra; and (iii) ascertaining the nature of the methylation of a dimethylarginine residue identifying in step (i) by determining if a neutral loss spectra of the sample peptide shows one or both of neutral loss of monomethylamine (MMA), dimethylcarbodiimide (DMC), and/or neutral loss of dimethylamine (DMA), wherein neutral loss of monomethylamine (MMA) and of dimethylcarbodiimide (DMC) indicates the presence of a symmetrically dimethylated arginine residue whereas neutral loss of dimethylamine (DMA) indicates the presence of a asymmetrically dimethylated arginine residue.

Summary of Invention Paragraph - BSTX (17):

[0016] In certain embodiments, the method further comprising determining the substrate specificity of a protein **arginine methyltransferase** by determining the sequence of at least that portion of a polypeptide including a dimethylarginine residue.

Detail Description Paragraph - DETX (3):

[0033] The present invention relates to the development of a mass spectrometry-based assay for protein **arginine methyltransferases** which can be used to differentiate between asymmetric and symmetric dimethylarginines in a protein substrate, and therefore between class I and class II PRMTs. The appended examples demonstrate in further detail that, for example, fragmentation of a peptide containing either symmetric dimethylarginine or

asymmetric dimethylarginine produces characteristic neutral losses that can be used to identify which type of dimethylarginine is present in a peptide sample.

Claims Text - CLTX (4):

3. A method for identifying substrates of a protein **arginine methyltransferase** comprising: (i) obtaining mass spectra for one or more sample polypeptides which have been exposed to a protein **arginine methyltransferase** (PRMT) under conditions wherein methylation, if any, of arginine residues in a substrate protein of the PRMT can occur; (ii) identifying the presence of dimethylarginine residues in the sample polypeptide by the presence of mass modified arginine in the mass spectra; and (iii) ascertaining the nature of the methylation of a dimethylarginine residue identifying in step (i) by determining if a neutral loss spectra of the sample peptide shows one or both of neutral loss of monomethylamine (MMA), dimethylcarbodiimide (DMC), and/or neutral loss of dimethylamine (DMA), wherein neutral loss of monomethylamine (MMA) and of dimethylcarbodiimide (DMC) indicates the presence of a symmetrically dimethylated arginine residue whereas neutral loss of dimethylamine (DMA) indicates the presence of a asymmetrically dimethylated arginine residue.

Claims Text - CLTX (5):

4. The method of claim 3, further comprising determining the substrate specificity of a protein **arginine methyltransferase** by determining the sequence of at least that portion of a polypeptide including a dimethylarginine residue.

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PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030082561 A1

TITLE: Zinc finger domain recognition code and uses thereof

PUBLICATION-DATE: May 1, 2003

INVENTOR-INFORMATION:

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non-provisional-of-provisional 60220060 20000721 US

US-CL-CURRENT: 435/6, 435/226 , 435/320.1 , 435/455 , 435/69.1 , 435/7.1

ABSTRACT:

The present invention relates to DNA binding proteins comprising zinc finger domains in which two histidine and two cysteine residues coordinate a central zinc ion. More particularly, the invention relates to the identification of a context-independent recognition code to design zinc finger domains. This code permits identification of an amino acid for positions -1, 2, 3 and 6 of the .alpha.-helical region of the zinc finger domain from four-base pair nucleotide target sequences. The invention includes zinc finger proteins (ZFPs) designed using this recognition code, nucleic acids encoding these ZFPs and methods of using such ZFPs to modulate gene expression, alter genome structure, inhibit viral replication and detect alterations (e.g., nucleotide substitutions, deletions or insertions) in the binding sites for such proteins. In addition, the invention provides a rapid method of assembling a ZFP with three or more zinc finger domains using three sets of 256 oligonucleotides, where each set is designed to target the 256 different 4-base pair targets and allow production of all possible 3-finger ZFPs (i.e., >>10.sup.6) from a total of 768 oligonucleotides. The invention also is directed to a method of preparing artificial transcription factors.

[0001] This application is a continuation-in-part application of U.S. Ser. No. 09/911,261, filed Jul. 23, 2001, which claims benefit of provisional application U.S. Serial No. 60/220,060, filed Jul. 21, 2000.

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Summary of Invention Paragraph - BSTX (67):
[0065] In a particular embodiment, a fusion protein has a first segment which is any ZFP of the invention, and a second segment comprising a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator,** a single-stranded DNA binding protein, a nuclear-localization signal, a transcription-protein recruiting protein or a cellular uptake domain. In an alternative embodiment, the second segments can comprise a protein domain which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear localization activity, transcriptional protein recruiting activity, **transcriptional repressor activity or transcriptional activator** activity. Those artificial ZFPs that can modulate gene expression, whether via a fused transcriptional effector domain or via a ZFP that acts to inhibit transcription by its DNA binding, are also referred to as artificial transcription factors (ATFs).

Summary of Invention Paragraph - BSTX (114):
[0112] The above-described methods for preparing ATFs are applicable for preparing, via the selection and/or screening process, any protein having a DNA-binding domain and having or controlling a predetermined biological activity. The contemplated methods are used with both a combinatorial library and a scanning library. In addition to having a DNA-binding domain, the proteins prepared by this method may comprise an effector domain. The effector domains can be any one described herein and include, but are not limited to, a transcriptional regulatory domain as well as a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator, single-stranded DNA binding protein, transcription** factor recruiting protein, nuclear-localization signal, cellular uptake signal or any combination thereof. Similarly, the effector domain can be a domain which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear-localization signaling activity, **transcriptional repressor activity, transcriptional activator** activity, single-stranded DNA binding activity, transcription factor recruiting activity, cellular uptake signaling activity or any combination of such activities.

Detail Description Paragraph - DETX (35):
[0198] In addition, the invention includes isolated fusion proteins comprising a ZFP of the invention fused to second domain (an effector domain)

which is a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repress r, transcriptional activator, single-stranded DNA binding pr tein, transcription** factor recruiting protein, nuclear-localization signal or cellular uptake signal. In an alternative embodiment, the second domain is a protein domain which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear-localization signaling activity, **transcriptional repressor activity, transcriptional activator** activity, single-stranded DNA binding activity, transcription factor recruiting activity, or cellular uptake signaling activity.

Detail Description Paragraph - DETX (121):

[0284] Likewise an effector domain can include, but is not limited to a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator,** a single-stranded DNA binding protein, a nuclear-localization signal, a transcription-protein recruiting protein or a cellular uptake domain. Effector domains further include protein domains which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear localization activity, transcriptional protein recruiting activity, **transcriptional repressor activity or transcriptional activator** activity.

Claims Text - CLTX (46):

42. The method of claim 37 or 38, wherein said effector domain comprises a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator, single-stranded DNA binding protein, transcription** factor recruiting protein, nuclear-localization signal, cellular uptake signal or any combination thereof.

Claims Text - CLTX (47):

43. The method of claim 37 or 38, wherein said effector domain comprises a domain which exhibits transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA **methyltransferase** activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear-localization signaling activity, **transcriptional repressor activity, transcriptional activator** activity, single-stranded DNA binding activity, transcription factor recruiting activity, cellular uptake signaling activity or any combination of such activities.

Claims Text - CLTX (60):

55. An isolated fusion protein comprising (a) a first segment which is a ZFP of claim 50, and (b) a second segment comprising a transposase, integrase, recombinase, resolvase, invertase, protease, DNA **methyltransferase,** DNA demethylase, histone acetylase, histone deacetylase, nuclease, **transcriptional repressor, transcriptional activator, single-stranded DNA binding protein, transcription** factor recruiting protein nuclear-localization signal or cellular uptake signal.

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PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030082552 A1

TITLE: Modulation of gene expression using localization domains

PUBLICATION-DATE: May 1, 2003

INVENTOR-INFORMATION:

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RELATED-US-APPL-DATA:

non-provisional-of-provisional 60236884 20000929 US

US-CL-CURRENT: 435/6, 435/317.1 , 435/455

ABSTRACT:

Methods and compositions for regulating gene expression are provided. In particular, methods and compositions comprising localization domains, and fusions of localization domains with DNA binding domains and, optionally regulatory domains, are provided.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is related to U.S. Provisional Patent Application Serial No. 60/236,884, filed Sep. 29, 2000, from which priority is claimed under 35 USC .sctn.119(e)(1), and which application is incorporated herein by reference in its entirety.

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Detail Description Paragraph - DETX (88):

[0118] Common regulatory domains for use in a fusion molecule include, e.g., effector domains from **transcripti n factors (activat rs,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene

transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20030082511

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030082511 A1

TITLE: Identification of modulatory molecules using inducible promoters

PUBLICATION-DATE: May 1, 2003

INVENTOR-INFORMATION:

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APPL-NO: 09/ 965201

DATE FILED: September 25, 2001

US-CL-CURRENT: 435/4, 435/6

ABSTRACT:

Methods for identifying an ion channel modulator, a target membrane receptor modulator molecule, and other modulatory molecules are disclosed, as well as cells and vectors for use in those methods. A polynucleotide encoding target is provided in a cell under control of an inducible promoter, and candidate modulatory molecules are contacted with the cell after induction of the promoter to ascertain whether a change in a measurable physiological parameter occurs as a result of the candidate modulatory molecule.

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Detail Description Table CWU - DETL (6):

1" ATP6EP2 "ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31 kD pseudogene 2" ATP6F "ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21 kD" ATP6G "ATPase, H+ transporting, lysosomal (vacuolar proton pump)" ATP6H "ATPase, H+ transporting, lysosomal (vacuolar proton pump) 9 kD" ATP6J "ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J; ATP6GL" ATP6N1A "ATP6N1; ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116 kD); VPP1; vacuolar proton pump, subunit 1" ATP6N2 "ATPase, H+ transporting, lysosomal (vacuolar proton pump) non- catalytic accessory protein 2 (38 kD)" ATP6S1 "ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1; ORF; XAP-3; VATPS1; 16A" ATP6S14 "ATPase, vacuolar, 14 kD" ATP7A "Hs.606; MNK; ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)" ATP7B "ATPase, Cu++ transporting, beta polypeptide (Wilson disease); Hs.84999; WND" ATPC2B

"ATPASEP; ATPase, class 2, member b; ATPase type IV, phospholipid transporting (P-type) (putative)" ATPP2 ATPASEII; aminophospholipid translocase ATRN attractin (with dipeptidylpeptidase IV activity) AUH AU RNA-binding protein/enoyl-Coenzyme A hydratase AXL Hs.83341; AXL receptor tyrosine kinase B3GALT1 "UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1; BETA3GAL-T1" B3GALT2 "beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S); BETA3GAL-T2; UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2; GlcAT-S" B3GALT3 "BETA3GAL-T3; UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3" B3GALT4 "BETA3GAL-T4; UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4" B3GALT5 "UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5; beta3Gal-T5" B4GALT1 GGTB2; Hs.80881; glycoprotein-4-beta-galacto-syltransferase 2 B4GALT2 "UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2; beta4Gal-T2" B4GALT3 "BETA4GAL-T3; UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3" B4GALT4 "BETA4GAL-T4; UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4" B4GALT5 "UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5; beta4GalT-V; beta4-GalT IV" B4GALT6 "UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6" B4GALT7 "xylosylprotein betal,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I); XGPT1; XGALT-1; beta4Gal-T7" B99 GTSE-1; Hs.122552; Gtsel (mouse) homolog; GTSE1; G two S phase expressed protein 1 BAAT BAT; bile acid Coenzyme A: amino acid N-acyltransferase (glycine N- choloyltransferase) BAP1 BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase); ubiquitin carboxy-terminal hydrolase BBOX "BBH; G-BBH; GAMMA-BBH; butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase)" BCAT1 "BCT1; branched chain aminotransferase 1, cytosolic" BCAT2 "BCT2; branched chain aminotransferase 2, mitochondrial" BCHE butyrylcholinesterase; E1; CHE1 BCHEL1 butyrylcholinesterase-like 1; CHEL1 BCHEL3 butyrylcholinesterase-like 3; CHEL3 BCKDHA "Hs.78950; branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease)" BCKDHB "Hs.1265; branched chain keto acid dehydrogenase E1, beta polypep- tide (maple syrup urine disease)" BCKDK branched chain aipha-ketoacid dehydrogenase kinase BCPM benign chronic pemphigus (Hailey-Hailey disease) BDH "3-hydroxybutyrate dehydrogenase (heart, mitochondrial)" BETA3GNT "beta-1,3-N-acetylglucosaminyltransferase" BETA3GNTI "i-beta-1,3-N-acetylglucosaminyltransferase" BHMT betaine-homocysteine methyltransferase BLK B lymphoid tyrosine kinase; Hs.2243 BLMH bleomycin hydrolase BLVRA BLVR; biliverdin reductase A BLVRB biliverdin reductase B BMPR1A "ACVRLK3; bone morphogenetic protein receptor, type IA; ALK3; activin A receptor, type II-like kinase 3" BMPR2 "bone morphogenetic protein receptor, type II (serine/threonine kinase); BRK-3; T-ALK; BMPR3; BMPR-II" BMX BMX non-receptor tyrosine kinase; ETK; PSCTK2 BPGM "Hs.79537; 2,3-bisphosphoglycerate mutase" BPHL biphenyl hydrolase-like (serine hydrolase); D0S2254E; MCNAA; Bph-rp BPNT1 "3'(2'), 5'-bisphosphate nucleotidase 1" BTD Hs.78885; biotinidase BTK Bruton agammaglobulinemia tyrosine kinase; ATK; XLA; IMD1; AGMX1; PSCTK1 CA1 Hs.23118; carbonic anhydrase I CA10 carbonic anhydrase X CA11 carbonic anhydrase XI; CARP2 CA12 carbonic anhydrase XII CA2 Hs.89748; carbonic anhydrase II; Hs.78883 CA3 "carbonic anhydrase III, muscle specific" CA4 carbonic anhydrase IV; Hs.89485; CAIV CA5A "CA5; carbonic anhydrase VA, mitochondrial; carbonic anhydrase V, mitochondrial; Hs.137; CAV; CAVA" CA5B "carbonic anhydrase VB, mitochondrial" CA5P carbonic anhydrase V pseudogene CA6 Hs.73855; carbonic anhydrase VI CA7 carbonic anhydrase VII CA8 carbonic anhydrase VIII; CALS;

CARP CA9 carbonic anhydrase IX; MN CAD "carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase" CALM1 "calmodulin 1 (phosphorylase kinase, delta); Hs.73785; CAMI; PHKD; DD132; CALML2" CALM1P1 "calmodulin 1 (phosphorylase kinase, delta) pseudogene 1" CALM1P2 "calmodulin 1 (phosphorylase kinase, delta) pseudogene 2" CALM2 "PHKD; CAMII; calmodulin 2 (phosphorylase kinase, delta)" CALM3 "PHKD; calmodulin 3 (phosphorylase kinase, delta)" CAMK1 calcium/calmodulin-dependent protein kinase I; CAMK1-PEN; CaMKI CAMK2A CAMKA; calciumlca/modulin-dependent protein kinase (CaM kinase) II alpha; KIAA0968 CAMK2B CAMKB; calciumlca/modulin-dependent protein kinase (CaM kinase) II beta CAMK2D CAMKD; calciumlca/modulin-dependent protein kinase (CaM kinase) II delta; CaMKII delta CAMK2G CAMKG; calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma CAMK4 calcium/calmodulin-dependent protein kinase IV; Hs.348 CAMKK1 "calcium/camodulin-dependent protein kinase kinase 1, alpha; CaMKKa" CAMK1K2 "calcium/calmodulin-dependent protein kinase kinase 2, beta; CaMKK; CaMKKb; KIAA0787" CANPX calpain-like protease CAP1 "CAP1-PEN; adenylyl cyclase-associated CAP protein, yeast homolog" CAP2 adenylyl cyclase-associated protein 2 CAPN7 calpain 7; calpain like protease; PalBH CARKL carbohydrate kinase-like CARM1 coactivator-associated **arginine methyltransferase**-1 CARS Hs.16642; cysteinyl-tRNA synthetase CASK calcium/calmodulin-depend- ent serine protein kinase (MAGUK family) CASKP calcium/calmodulin-dependent serine protein kinase (MAGUK family) pseudogene CASP1 "IL1BC; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); Hs.2490; ICE" CASP10 "caspase 10, apoptosis-related cysteine protease; MCH4" CASP13 "caspase 13, apoptosis-related cysteine protease; ERICE" CASP2 "NEDD2; caspase 2, apoptosis-related cysteine protease (neural pre- cursor cell expressed, developmentally down-regulated 2); ICH1" CASP3 "CPP32B; caspase 3, apoptosis-related cysteine protease; Yama; CPP32; apopain" CASP4 caspase 4, apoptosis-related cysteine protease; TX; ICH-2; ICErel-II" CASP5 "caspase 5, apoptosis-related cysteine protease; ICErel-III" CASP6 "caspase 6, apoptosis-related cysteine protease; MCH2" CASP7 "caspase 7, apoptosis-related cysteine protease; MCH3; CMH-1; ICE- LAP3"

Detail Description Table CWU - DETL (17):

"phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase carboxylase pseudogene 1" PAICSP2 "phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase pseudogene 2" PAK1 p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related) PAK2 p21 (CDKN1A)-activated kinase 2; hPAK65 PAK3 "MRX30; p21 (CDKN1A)-activated kinase 3; mental retardation, X- linked 30; bPAK; hPAK3" PAK4 "protein kinase related to S. cerevisiac STE20, effector for Cdc42Hs" PAM Hs.83920; peptidylglycine alpha-amidating monooxygenase PAP poly(A) polymerase PAPSS1 3'-phosphoadenosine 5'-phosphosulfate synthase 1; PAPSS; ATPSK1 PAPSS2 SK2; ATPSK2; 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 2 PARG poly (ADP-ribose) glycohydrolase PARK2 "Parkinson disease (autosomal recessive, juvenile) 2; PDJ; AR-JP; parkin" PARK3 "Parkinson disease, dominant Lewy-body, 3" PARN poly(A)-specific ribonuclease (deadenylation nuclease) PC Hs.89890; pyruvate carboxylase; PCB PC4 PC4-LSB; activated RNA polymerase II **transcription cofactor; activated** RNA polymerase II transcription cofactor 1; activated RNA polymerase II transcription cofactor 4; P15 PCBD Hs.3192; PCD; DCOH; 6-pyruvoyl-tetrahydropterin synthase/dimeriza- tion cofactor of

hepatocyte nuclear factor 1 alpha (TCF1); pterin-4 -alpha carbinolamine dehydratase PCCA "Hs.80741; propionyl Coenzyme A carboxylase, alpha polypeptide" PCCB "Hs.63788; propionyl Coenzyme A carboxylase, beta polypeptide" PCK1 Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble) PCK2 PEPCK; phosphoenolpyruvate carboxykinase 2 (mitochondrial) PCLD PLD1; polycystic liver disease; PLD PCMT1 protein-L-isoaspartate (D-aspartate) **O-methyltransferase** PCOLC procollagen C-endopeptidase PCOLCE procollagen C-endopeptidase enhancer; Hs.91299 PCOLN3 procollagen (type III) N-endopeptidase PCSK1 Hs.78977; PC1; NEC1; PC-1; proprotein convertase subtilisin/kexin type 1 PCSK2 Hs.93164; PC2; NEC2; PC-2; proprotein convertase subtilisin/kexin type 2 PCSK3 proprotein convertase subtilisin/kexin type 3 PCSK4 PC4; proprotein convertase subtilisin/kexin type 4 PCSK5 proprotein convertase subtilisin/kexin type 5 PCSK7 PC8; PC7; LPC; SPC7; proprotein convertase subtilisinlkexin type 7; Lymphoma Proprotein Convertase PCTK1 1; PCTGAIRE; PCTAIRE protein kinase 1 PCTK2 PCTAIRE protein kinase 2 PCTK3 Hs.2994; 3; PCTAIRE; protein kinase 3 PCYT1A "PCYT1; phosphate cytidylyltransferase 1, choline; CT; CTPCT" PCYT1B "CCT-BETA; phosphate cytidylyltransfearse 1, choline; beta isoform" PCYT2 "phosphate cytidylyltransferase 2, ethanolamine; ET" PDB1 PDB; Paget disease of bone 1 PDB2 Paget disease of bone 2 PDE10A phosphodiesterase 10A PDE1A "phosphodiesterase 1A, calmodulin-dependent; Hs.41717; Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1A3A)" PDE1B "PDES1B; phosphodiesterase 1B, calmodulin-dependent" PDE1C "phosphodiesterase 1C, calmodulin-dependent (70 kD); HCAM3; Hs.41718; Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE1C1A)" PDE2A "phosphodiesterase 2A, cGMP-stimulated; Hs.3831; Human cGMP- stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA, complete cds" PDE3A "phosphodiesterase 3A, cGMP-inhibited; CGI-PDE" PDE3B "phosphodiesterase 3B, cGMP-inhibited" PDE4A "Hs.96083; DPDE2; phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)" PDE4B "Hs.188; DPDE4; PDEIVB; phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)" PDE4C "Hs.189; DPDE1; phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1)" PDE4D "DPDE3; phosphodiesterase 4D, cAMP-specific (dunce (Drosophila)- homolog phosphodiesterase E3)" PDE5A "phosphodiesterase SA, cGMP-specific" PDE6A "phosphodiesterase 6A, cGMP-specific, rod, alpha; PDEA" PDE6B "phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant); Hs.2593; CSNB3; PDEB" PDE6C "phosphodiesterase 6C, cGMP-specific, cone, alpha prime" PDE6D "phosphodiesterase 6D, cGMP-specific, rod, delta" PDE6G "phosphodiesterase 6G, cGMP-specific, rod, gamma; Hs.1857; PDEG" PDE6H "phosphodiesterase 6H, cGMP-specific, cone, gamma" PDE7A phosphodiesterase 7A; HCP1 PDE8A phosphodiesterase 8A PDE8B phosphodiesterase 8B PDE9A phosphodiesterase 9A PDHA1 Hs.1023; PDHA; pyruvate dehydrogenase (lipoamide) alpha 1 PDHA2 PDHAL; pyruvate dehydrogenase (lipoamide) alpha 2 PDHB Hs.979; pyruvate dehydrogenase (lipoamide) beta PDI PDI-PEN; protein disulfide isomerase(pancreas) PDI2 "KIAA0994; peptidyl arginine deiminase, type II" PDIR for protein disulfide isomerase-related PDK1 "pyruvate dehydrogenase kinase, isoenzyme 1; Hs.81233" PDK2 "pyruvate dehydrogenase kinase, isoenzyme 2" PDK3 "pyruvate dehydrogenase kinase, isoenzyme 3" PDK4 "pyruvate dehydrogenase kinase, isoenzyme 4; Hs.57695" PDNP1 NPPS; M6S1; PC-1; phosphodiesterase I/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen) PDNP2 ATX; phosphodiesterase I/nucleotide pyrophosphatase 2 (autotaxin); autotaxin; PD-IALPHA PDNP3 phosphodiesterase I/nucleotide

pyrophosphatase 3; PD-IBETA PDPK1 PDK1; PkB kinase PDX1 "pyruvate dehydrogenase complex, component X; protein X" PDXK "pyridoxal (pyridoxine, vitamin B6) kinase; PKH; PNK" PECI "peroxisomal D3,D2-enoyl-CoA isomerase" PEMT phosphatidylethanolamine N-**methyltransferase**; PEMT2; PEMPT PEN11B putative serine/threonine protein kinase PEPA peptidase A PEPB peptidase B PEPC peptidase C PEPD Hs.73947; peptidase D PEPE peptidase E PEPS peptidase S PFAS phosphoribosylformylglycinamidine synthase (FGAR amidotransferase); A putative Human homolog of PHOSPHORIBOSYLFORMYLGLYCINAMIDE SYNTHASE; PURL;

KIAA0361; FGARAT PFKFB1 "Hs.739; PFRX; 6-phosphoftucto-2-kinase/fructose-2,6-biphosphatase 1" PFKFB2 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2" PFKFB3 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3" PFKFB4 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4" PFKL "phosphofructokinase, liver; Hs.100005" PFKM "Hs.75160; phosphofructokinase, muscle" PFKP "Hs.99910; phosphofructokinase, platelet; Hs.75363" PFKX "phosphofructokinase polypeptide X" PFTK1 PFTAIRE protein kinase 1 PGAM1 Hs.74575; PGAMA; phosphoglycerate mutase 1 (brain) PGAM2 Hs.46039; phosphoglycerate mutase 2 (muscle) PGCP plasma glutamate carboxypeptidase PGD Hs.75888; phosphogluconate dehydrogenase PGDL1 phosphogluconate dehydrogenase-like 1 PGGT1B "protein geranylgeranyltransferase type I, beta subunit; GGTI; BGGI" PGK1 Hs.78771; phosphoglycerate kinase 1 PGK1P1 "phosphoglycerate kinase 1, pseudogene 1" PGK1P2 "phosphoglycerate kinase 1, pseudogene 2" PGK2 phosphoglycerate kinase 2 PGM1 phosphoglucomutase 1; Hs.1869 PGM2 phosphoglucomutase 2 PGM3 phosphoglucomutase 3 PGM5 phosphoglucomutase 5 PGP phosphoglycolate phosphatase PGS1 Phosphatidylglycerophosphate Synthase PHEX "HYP; phosphate regulating gene with homologies to endopeptidases on the X chromosome (hypophosphatemia, vitamin D resistant rickets); PEX; HPDR" PHGDH phosphoglycerate dehydrogenase; PGAD; 3-phosphoglycerate dehydrogenase; PDG; PGDH; SERA PHKA1 "phosphorylase kinase, alpha 1 (muscle); Hs.2393; PHKA; phosphorylase kinase, alpha 1 (muscle), muscle glycogenosis" PHKA2 "PHK; phosphorylase kinase, alpha 2 (liver); phosphorylase kinase deficiency, liver (glycogen storage disease type VIII); PYK; XLG; XLG2; PYKL; phosphorylase kinase, alpha 2 (liver), glycogen storage disease IX" PHKB "phosphorylase kinase, beta" PHKBP1 "phosphorylase kinase, beta pseudogene 1" PHKBP2 "phosphorylase kinase, beta pseudogene 2" PHKG1 "PHKG; phosphorylase kinase, gamma 1 (muscle)" PHKG2 "Hs.87452; phosphorylase kinase, gamma 2 (testis)" PHKGL "phosphorylase

Detail Description Table CWU - DETL (26):

3TABLE III Name DNA Binding Protein Description ALRP ankyrin-like repeat protein; CARP; C-193; cytokine inducible nuclear protein; cardiac ankyrin repeat protein APEG1 "nuclear protein, marker for differentiated aortic smooth muscle and down-regulated with vascular injury" APEX APE; APEX nuclease (multifunctional DNA repair enzyme); REF1; HAP1; apurinic/apyrimidinic (abasic) endonuclease ARNT aryl hydrocarbon receptor nuclear translocator; Hs.47477; HIF1beta ARNTL aryl hydrocarbon receptor nuclear translocator-like; MOP3; JAP3; BMAL1 B4-2 proline-rich protein with nuclear targeting signal BLZF1 JEM1; basic leucine zipper nuclear factor 1 (JEM-1) C1D nuclear DNA-binding protein C1D nuclear DNA-binding protein CHD1 chromodomain helicase DNA binding protein 1 CHD1L CHDL; CHD1L-PENDING; chromodomain helicase DNA binding protein 1-like CHD2 chromodomain helicase DNA binding

protein 2 CHD3 chromodomain helicase DNA binding protein 3; Mi-2a CHD4 chromodomain helicase DNA binding protein 4; Mi-2b DAP10 DNAX-activation protein 10 DDB1 Hs.74623; damage-specific DNA binding protein 1 (127 kD) DDB2 Hs.77602; damage-specific DNA binding protein 2 (48 kD) DDX9 "DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II); NDHII" DDX9 "DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II); NDHII" DDXL "nuclear RNA helicase, DECD variant of DEAD box family" DEK DEK oncogene (DNA binding); D6S231E DFFA "DNA fragmentation factor, 45 kD, alpha subunit" DFFB "DNA fragmentation factor, 40 kD, beta polypeptide (caspase-activated DNase); DNA fragmentation factor, 40 kD, beta subunit; CAD; DFF2; CPAN; DFF40; DFF-40" DMC1 "DMC1 (dosage suppressor of mck1, yeast homolog) meiosis-specific homologous recombination; DMC1H; disrupted meiotic cDNA 1 homolog; LIM15" DNA2L "DNA2 (DNA replication helicase, yeast, homolog)-like" DNAH11 "DNAHC11; dynein, axonemal, heavy chain 11" DNAH12 DHC3; HL19; HDHC3; HL-19; DNAHC3; DNAHC12; dynein heavy chain 12 DNASE2 "DNL2; deoxyribonuclease II, lysosomal; DNL; DNase II, lysosomal" ENC1 "NRPB; nuclear restricted protein, BTB domain-like (brain); PIG10; NRP/B" FBRNP heterogeneous nuclear protein similar to rat helix destabilizing protein GADD45A DDIT1; Hs.80409; GADD45; DNA-damage-inducible transcript 1 GADD45G "CR6; GADD45-GAMMA; growth arrest and DNA-damage-inducible, gamma" GRLF1 GRF-1; **glucocorticoid receptor** DNA binding factor 1 HDGF hepatoma-derived growth factor (high-mobility group protein 1-like); HMG1L2 HIRIP4 DNAJ; HIRA interacting protein 4 (dnaJ-like) HLJ1 DNAJW; DnaJ-like heat shock protein 40 HMG1 high-mobility group (nonhistone chromosomal) protein 1; HMG3; Hs.74570 HMG1L1 HMG1L7; high-mobility group (nonhistone chromosomal) protein 1-like 1 HMGCS1 Hs.21808; HMGCS; 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) HMGIY high-mobility group (nonhistone chromosomal) protein isoforms I and Y; Hs.64605; HMGI-Y; HMGI/Y HNF3A "hepatocyte nuclear factor 3, alpha" HNF3B "hepatocyte nuclear factor 3, beta" HNF3G "hepatocyte nuclear factor 3, gamma" HNF4A "TCF14; hepatic nuclear factor 4, alpha" HNF4B "hepatocyte nuclear factor 4, beta" HNF4G "hepatocyte nuclear factor 4, gamma" HNF6 hepatocyte nuclear factor 6 HNF6A "hepatocyte nuclear factor 6, alpha" HRIHFB2122 putative nuclear protein HSJ1 "heat shock protein, neuronal DNAJ-like, 1; HSPF3" HSJ2 "heat shock protein, DNAJ-like 2; HSPF4; dj-2; hdj-2" ID1 "Hs.75424; inhibitor of DNA binding 1, dominant negative helix-loop- helix protein" ID2 "inhibitor of DNA binding 2, dominant negative helix-loop-helix protein; Hs.76667" ID3 "Hs.76884; HEIR-1; inhibitor of DNA binding 3, dominant negative helix-loop-helix protein" ID4 "Hs.34853; inhibitor of DNA binding 4, dominant negative helix-loop- helix protein" INSL Insulin-like DNA sequence KIAA0765 HRIHFB2091; putative brain nuclearly-targeted protein KIP2 DNA-dependent protein kinase catalytic subunit-interacting protein 2 LAF4 lymphoid nuclear protein 4 LHFP lipoma HMGIC fusion partner LHFPL1 lipoma HMGIC fusion partner-like 1 LHFPL3 lipoma HMGIC fusion partner-like 3 LHFPL4 lipoma HMGIC fusion partner-like 4 LIG1 "Hs.1770 ligase I, DNA, ATP-dependent" LIG2 "ligase II, DNA, ATP-dependent" LIG3 "Hs.100299; ligase III, DNA, ATP-dependent" LIG4 "ligase IV, DNA, ATP-dependent" LPSA "Oncogene liposarcoma (DNA segment, single copy, expressed, probes" LXR "orphan nuclear hormone receptor, retinoid response" M96 putative DNA binding protein MERR metalloregulatory DNA-binding protein MGMT O-6-methylguanine-DNA **methyltransferase**; Hs.1384 MNDA Hs.3197; myeloid cell nuclear differentiation antigen MPG Hs.79396; MDG; N-methylpurine-DNA glycosylase MRJ MRJ gene for a member of the DNAJ protein family NAGR1 N-acetylglucosamine receptor 1

(thyroid); heterogenous nuclear ribonucleoprotein M4 NASP Hs.68875; nuclear autoantigenic sperm protein (histone-binding) NCBP "Hs.89750; nuclear cap binding protein, 80 kD; Hs.89563" NCOA1 nuclear receptor coactivator 1; SRC1; **ster id recept r** coactivator 1; NCoA-1; F-SRC-1 NCOA3 nuclear receptor coactivator 3; AIB1; ACTR; RAC3; p/CIP; CAGH16; TNRC16; TRAM-1; amplified in breast cancer 1 NCOA4 nuclear receptor coactivator 4; RFG; ELE1; ARA70 NCOR1 nuclear receptor co-repressor 1; N-CoR; TRAC1; hN-CoR; KIAA1047; hCIT529I10 NCOR2 nuclear receptor co-repressor 2; SMRT; CTG26; SMRTE; TNRC14; TRAC-1 NCYM DNA-binding **transcriptional activator** NDP52 nuclear domain 10 protein NDR "NDR-LSB; serine/threonine kinase, nuclear Dfnb2-related (Drosophila) homolog" NFAT5 nuclear factor of activated T-cells 5; TONEBP; KIAA0827 NFATC1 "nuclear factor of activated T-cells, cytoplasmic 1; NF-ATC" NFATC2 "NF-ATP; nuclear factor of activated T-cells, cytoplasmic 2" NFATC3 "NFAT4; NFATX; nuclear factor of activated T-cells, cytoplasmic 3" NFATC4 "NFAT3; nuclear factor of activated T-cells, cytoplasmic 4" NFATC5 "nuclear factor of activated T-cells, cytoplasmic 5" NFE2 "NF-E2; nuclear factor (erythroid-derived 2), 45 kD" NFE2L1 nuclear factor (erythroid-derived 2)-like 1; NRF1; LCR-F1 NFE2L2 NRF2; nuclear factor (erythroid-derived 2)-like 2 NFE2L3 NRF3; nuclear factor (erythroid-derived 2)-like 3 NFIA KIAA1439; NFI-L; nuclear factor I/A NFIB NFI-RED; nuclear factor I/B NFIC NFI; CTF; NF-I; nuclear factor I/C (CCAAT-binding transcription factor) NFIL3 "IL3BP1; nuclear factor, interleukin 3 regulated; E4BP4; NFIL3A; NF- IL3A" NFIX Hs.99929; nuclear factor I/X (CCAAT-binding transcription factor) NFIXL1 nuclear factor I/X-like 1 NFIXL2 nuclear factor I/X-like 2 NFIXL3 nuclear factor I/X-like 3 NFIXL4 NFIX; nuclear factor I/X-like 4 NFIXL5 nuclear factor I/X-like 5 NFKB1 Hs.83428; KBF1; nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) NFKB2 Hs.73090; LYT-10; nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) NFKBIA "NFKBI; nuclear factor of kappa light polypeptide gene enhancer in B- cells inhibitor, alpha; IKBA; MAD-3" NFKBIB "nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta; IKBB; TRIP9" NFKBIE "nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon; IKBE" NFKBIL1 IKBL; NFKBIL; nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1 NFKBIL2 IKBR; nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2 NFRKB nuclear factor related to kappa B binding protein NFX1 "nuclear transcription factor, X-box binding 1" NFYA "nuclear transcription factor Y, alpha; Hs.797; HAP2; CBF-A" NFYB "nuclear transcription factor Y, beta; CBF-B" NFYC "nuclear transcription factor Y, gamma; CBF-C" NIP1 NIP1-PEN; Nuclear cap binding protein (NCBP) interacting protein-1 NIP1L "nip1 (nuclear import protein, S cerevisiae)-like" NLVCF nuclear localization signal deleted in velocardiofacial syndrome NR1D1 "EAR-1; THRAL; REV-ERBAALPHA; nuclear receptor subfamily 1, group D, member 1" NR1D2 "RVR; BD73; HZF2; EAR-1R; nuclear receptor subfamily 1, group D, member 2" NR1H2 UNR; ubiquitously-expressed nuclear receptor NR1H3 "LXRA; LXR-A; RLD-1; NR1H3-PENDING; nuclear receptor subfamily 1, group H, member 3" NR1H4 "FXR; HRR1; RIP14; NR1H4-PENDING; nuclear receptor subfamily 1,

PGPUB-DOCUMENT-NUMBER: 20030077664

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030077664 A1

TITLE: Methods of screening for compounds that modulate hormone receptor activity

PUBLICATION-DATE: April 24, 2003

INVENTOR-INFORMATION:

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Chandraratna, Roshantha A.	Laguna Hills	CA	US	

APPL-NO: 09/ 922226

DATE FILED: August 2, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60284797 20010418 US

US-CL-CURRENT: 435/7.2

ABSTRACT:

The present invention provides methods for identifying an effective agent that modulates a biological activity of a nuclear hormone receptor. In a method of the invention, an isolated receptor-containing complex is assayed for an altered modification state as compared to a control modification state. The presence of an altered modification state serves to identify an effective agent that modulates a biological activity of the nuclear hormone receptor.

[0001] This application is based on, and claims the benefit of, U.S. Provisional Application No. 60/284,797, filed Apr. 18, 2001, and entitled NOVEL METHODS OF SCREENING FOR COMPOUNDS THAT MODULATE HORMONE RECEPTOR
ACTIVITY, and which is incorporated herein by reference.

---------- KWIC ---------

Detail Description Paragraph - DETX (85):
[0129] Additional protein kinase A substrates useful in the invention include but are not limited to the following: acetyl-CoA carboxylase;

acetyl-CoA carboxylase kinase; arylsulfatase B; ATP citrate lyase; cholesterol esterase; cyclic nucleotide phosphodiesterase; erythrodihydroneopterin triphosphate synthetase; F 1-ATPase precursor; fructose-1,6-bisphosphatase; fructose-2,6-bisphosphatase/fructose-6-phosp- hate-2-kinase; muscle fructose-6-phosphate-1-kinase; liver fructose-6-phosphate-1-kinase; muscle glycogen synthase; liver glycogen synthase; guanylate cyclase; hormone-sensitive lipase/diglyceride lipase; myosin light-chain kinase; Na.sup.+, K.sup.+-ATPase, .alpha.-subunit; phenylalanine hydroxylase; phospholipid **methyltransferase**; phosphorylase kinase; pyruvate kinase, liver; erythrocyte pyruvate kinase; RNA polymerase; PKA Catalytic subunit; PKA Regulatory subunit (R.sup.II); threonyl-tRNA synthetase; or tyrosine hydroxylase, and fragments of any of the above proteins. Protein kinase A substrates useful in the invention further include, for example, actin; atrial natriuretic peptides; calciductin; dihydropyridine-sensitive calcium channel; choriogonadotropin; collagen, .alpha.I; cytochrome P-450 LM2; fibrinogen; filamin; G-substrate; glicentin; **glucocorticoid receptor**; histone; HMG 14; keratin proteins; lens .alpha.-crystallin; lipomodulin; MAP-2; myelin basic protein; phosphatase inhibitor 1; phospholamban; prolactin; ribosomal protein S6; sodium channel .alpha.-subunit; or cardiac or skeletal muscle troponin I, and fragments of any of the above proteins (Zetterqvist et al., supra, 1990). It is understood that these and other protein kinase A substrates known in the art can be useful in the methods of the invention, and further that routine methods can be used to identify additional protein substrates, fragments thereof, or synthetic substrates.

PGPUB-DOCUMENT-NUMBER: 20030073197

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030073197 A1

TITLE: Methyltransferase gene and enzyme

PUBLICATION-DATE: April 17, 2003

INVENTOR-INFORMATION:

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APPL-NO: 10/ 273769

DATE FILED: October 18, 2002

RELATED-US-APPL-DATA:

child 10273769 A1 20021018

parent division-of 09296840 19990422 US GRANTED

parent-patent 6492168 US

non-provisional-of-provisional 60082674 19980422 US

US-CL-CURRENT: 435/69.1, 424/93.2 , 435/193 , 435/235.1 , 435/257.3 , 536/23.2

ABSTRACT:

A novel cytosine-5 DNA methyltransferase, isolated from Chlorella virus NYs-1, and its encoded enzyme are disclosed. The methyltransferase recognizes a GpC dinucleotide in DNA. Methods of using the novel methyltransferase in high resolution chromatin mapping and related techniques are also disclosed.

[0001] This application claims priority to U.S. Provisional Application Serial No. 60/082,674, filed Apr. 22, 1998, which is incorporated by reference herein.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (5):

[0005] In vivo methylation of DNA has been used successfully to study protein-DNA interactions in the chromatin of living cells. A high frequency of

methyltransferase targets is critical for high resolution mapping of chromatin structure. Among currently available **methyltransferase** probes, the only de novo dinucleotide **methyltransferase** is M.SssI, which recognizes a CpG site (Renbaum, P., Abrahamove, D., Fainsod, A., Wilson, G., Rottem, S. and Razin, A. (1990) Nucleic Acids Res., 18, 1145-1152). Due to under-representation of the CpG dinucleotide in the genome, the resolution of chromatin structure maps using this enzyme is about 35 base pairs on average in S. cerevisiae (Dujon, B., Alexandrakl, D., Andr, B., Ansorge, W., Baladron, V., Ballesta, J. P. G., Banrevl, A., Bolle, P. A., Bolotin-Fukuhara, M., Bossler, P. et al). (1994) Nature, 369, 371-378.). With this moderate level of resolution, M.SssI can possibly serve to detect the presence of a positioned nucleosome, 146 bp in yeast, without the need for introduction of additional CpG sites into native DNA sequences. However, this resolution is insufficient for mapping the interactions of non-histone regulatory proteins, since the typical length of the target DNA sequence of most regulatory proteins is .about.20-30 base pairs or less. For example, the yeast TATA box binding protein (TBP) recognizes and binds to an 8 bp sequence (Kim, Y., Geiger, J. H., Hahn, S. and Sigler, P. B. (1993) Nature, 365, 512-520.), while the well-characterized **transcriptional activator** Gal4p binds to a 17 bp consensus sequence (Giniger, E., Varnum, S. M. and Ptashne, M. (1985) Cell, 40, 767-774.). Furthermore, methylation of CpG islands has been implicated as an important controlling element for gene regulation in mammalian systems, which may limit the application of M.SssI in higher organisms (Tazi, J. and Bird, A. (1990) Cell, 60, 909-920.). To address both the limitation of resolution and the possible inability to utilize M.SssI in higher organisms, cloning and expression of cytosine-5-DNA **methyltransferases** (5-.sup.meC MTase) with different specificities but similarly small recognition sites is essential.

PGPUB-DOCUMENT-NUMBER: 20030073163

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030073163 A1

TITLE: Libraries of expressible gene sequences

PUBLICATION-DATE: April 17, 2003

INVENTOR-INFORMATION:

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RELATED-US-APPL-DATA:

child 10003021 A1 20011114

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non-provisional-of-provisional 60096981 19980818 US

non-provisional-of-provisional 60080626 19980403 US

US-CL-CURRENT: 435/69.1, 435/183 , 435/193 , 435/320.1 , 435/325 , 435/6 , 536/23.2

ABSTRACT:

The invention described herein comprises libraries of expressible gene sequences. Such gene sequences are contained on plasmid vectors designed to endow the expressed proteins with a number of useful features such as affinity purification tags, epitope tags, and the like. The expression vectors containing such gene sequences can be used to transfect cells for the production of recombinant proteins. A further aspect of the invention comprises methods of identifying binding partners for the products of such expressible gene sequences.

RELATED APPLICATIONS

[0001] This application relies for priority on U.S. Provisional Application No. 60/080,626, filed Apr. 3, 1998, and U.S. Provisional Application No. 60/096,981, filed Aug. 18, 1998, each of which is hereby incorporated herein in its entirety.

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Detail Description Table CWU - DETL (51):
protein phosphatase 2C alpha 42.13 52.0 kDa [human, teratocarcinoma, mRNA, 2346 nt] M472 B1 H-U00803 tyrosine-protein kinase FRK 55.620 64.0 kDa B2 H-U02390 Human adenylyl cyclase- 52.58 55 associated protein homolog CAP2 (CAP2) mRNA, complete cds 167-2 H-U02680 human protein tyrosine kinase 36 38.57 mRNA G2 H-U03056 Human tumor suppressor (LUCA- 47.96 47 1) mRNA, complete cds M512 E3 H-U03100 Human alpha2(E)-catenin mRNA, 102.52 102.0 kDa complete cds M306 G3 H-U03187 72.93 95.0 kDa H3 H-U03398 Human receptor 4-1BB ligand 28.05 51 mRNA, complete cds D3 H-U03486 Human connexin40 gene, 39.49 40 complete cds M300 C3 H-U03643 leukophysin 25.96 34 F5 H-U03749 Human chromogranin A (CHGA) 50.38 50 gene, promoter and M314 C3 H-U03886 GS2 (GB: U03886) 27.94 32.0 kDa M306 E3 H-U04343 CD86 antigen (CD28 antigen 35.64 47 ligand 2, B7-2 antigen) [CD86] 167-61 H-U05012 TrkC 92 90.82 M302 G5 H-U05340 cell division cycle protein p55 55 55 A4 H-U05659 Hydroxysteroid (17-beta) 34.21 36 dehydrogenase 3 F1 H-U05861 Human hepatic dihydrodiol 35.64 40 dehydrogenase gene M302 B2 H-U06452 antigen MART-1, melanoma 13.09 20.0 kDa 169-52 H-U06454 human AMP-activated protein 70 60.79 kinase (hAMPK) mRNA M315 A3 H-U06643 lectin, epidermal 15.07 18 H1 H-U06715 Cytochrome B561 27.06 25 M476 E5 H-U07132 Human steroid hormone receptor 50.82 55.0 kDa Ner-l mRNA, complete cds M236 D3 H-U07151 guanine nucleotide-binding 20.13 34 protein ADP-ribosylation factor like gene 3 M317 G3 H-U07559 homeotic protein Islet-1 38.17 38 M266 H1 H-U07681 Human NAD(H)-specific 40.37 40 isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds E3 H-U07919 Aldehyde dehydrogenase 6 56.43 53 M298 A3 H-U08021 nicotinamide N-**methyltransferase** 29.15 36.0 kDa M297 B1 H-U08024 alcohol/hydroxysteroid 31.46 50.0 kDa sulfotransferase A2 H-U08336 Human basic helix-loop-helix 21.89 42 transcription factor mRNA, complete cds E2 H-U09303 Human T cell leukemia LERK-2 38.17 40 (EPLG2) mRNA, complete cds M250 H5 H-U09559 RCH1, RAG (recombination 58.3 58.0 kDa activating gene) cohort 1 167-50 H-U09564 human serine kinase mRNA 72 72.12 166-74 H-U09578 human MAPKAP kinase (3pK) 50 42.09 mRNA M302 C4 H-U09813 ATP synthase, subunit 9, 15.73 30 mitochondrial A1 H-U09850 Zinc finger protein 143 (clone 68.97 68 pHZ-1) M423 E1 H-U09937 Human urokinase-type 36.96 49.0 kDa plasminogen receptor M450 H4 H-U10117 Human endothelial-monocyte 34.43 38.0 kDa activating polypeptide II mRNA, complete cds M314 G1 H-U10248 ribosomal protein L29 17.6 27 M298 H1 H-U10323 nuclear factor 45 44.77 45 E1 H-U10492 Human Mox1 protein (MOX1) 28.05 37 mRNA, complete cds F3 H-U10686 Human MAGE-11 antigen 35.2 35 (MAGE11) gene, complete cds 167-38 H-U11050 human NIMA-like protein kinase 55 49.02 1 (NLK1) mRNA M266 B2 H-U11292 Human Ki nuclear autoantigen 29.48 32 mRNA, complete cds, may play a rol in cell adhesion 167-62 H-U11791 human cyclin H mRNA 40 35.60 M423 D5 H-U12255 immunoglobulin gamma heavy 40.26 48.0 kDa chain Fc receptor RI, high affinity M302 F7 H-U12404 Csa-19 23.98 32 M236 A2 H-U12465 ribosomal protein L35 13.64 24 169-4 H-U12535 human epidermal growth factor 100 90.49 receptor kinase substrate (Eps8) mRNA F3 H-U12597 Human tumor necrosis factor type 55.22 64 2 receptor associated protein (TRAP3) mRNA, complete cds M314 D1 H-U12979 **transcripti nal coactivator** PC4 14.08 23 M476 G4 H-U13044 GA-binding protein transcription 50.05 53.0 kDa factor, alpha subunit (60 kD) M302 F3 H-U13665 cathepsin O (GB: U13665) 36.3 50.0 kDa M311 G4 H-U13831 cellular retinol

binding protein II 14.85 20.0 kDa A2 H-U13991 Human TATA-binding protein 24.09 34 associated factor 30 kDa subunit (tafII30) mRNA, complete cds M416 A4 H-U14187 Human receptor tyrosine kinase 26.29 29.0 kDa ligand LERK-3 (EPLG3) mRNA, complete cds M250 A2 H-U14188 eph-related receptor tyrosine 22.22 27 kinase ligand 4 [EPLG4] M302 D2 H-U14193 human TFIIA gamma subunit 12.060 28.0 kDa mRNA M416 G1 H-U14603 Human protein-tyrosine 18.48 30.0 kDa phosphatase (HU-PP-1) mRNA, partial sequence E2 H-U14747 Visinin-like 1 21.12 25 M266 D4 H-U14966 ribosomal protein L5 32.78 38 M314 E2 H-U14967 ribosomal protein L21 17.71 29 M266 F5 H-U14968 ribosomal protein L27a 16.39 19.0 kDa M248 E3 H-U14969 ribosomal protein L28 15.18 27 M266 E1 H-U14971 ribosomal protein S9 21.45 30 M250 C2 H-U15009 small nuclear ribonucleoprotein, 13.97 17.0 kDa Sm D3 M311 D4 H-U16660 enoyl-Coenzyme A hydratase-like 36.19 38 protein, peroxisomal M302 H4 H-U17074 cyclin-dependent kinase 6 18.59 29 inhibitor p18 M306 A2 H-U17195 A-kinase anchor protein 100 72.05 100 [AKAP100*] D1 H-U17280 Steroidogenic acute regulatory 31.46 35 protein M316 F1 H-U18291 cell division cycle protein 16 68.2 71.0 kDa C5 H-U18420 Human ras-related small GTP 23.87 33 binding protein Rab5 (rab5) mRNA, complete cds M311 A2 H-U18423 spinal muscular atrophy gene 32.45 41 M248 D4 H-U18914 hypothetical protein, (Human 20.35 32 19.8 kDa protein mRNA, complete cds) M302 B5 H-U19718 microfibril-associated 20.24 34.0 kDa glycoprotein 2 M305 E3 H-U20240 CCAAT/enhancer-binding protein 16.61 29 gamma M302 A8 H-U20352 malate dehydrogenase 36.85 40 M416 F4 H-U20391 Human folate receptor (FOLR1) 28.38 34.0 kDa gene, complete cds M311 D1 H-U20536 apoptotic cysteine protease Mch2 32.34 38.0 kDa M431 G2 H-U20659 RNA polymerase II, subunit B7 19.03 31.0 kDa M499 C1 H-U20938 Human lymphocyte 112.86 100.0 kDa dihydropyrimidine dehydrogenase mRNA, complete cds M305 F2 H-U20972 14-3-3 protein, epsilon 28.16 36 M271 D3 H-U21049 hypothetical protein 12.65 16 (GB: U21049), ESTs, Highly similar to DD96 [H.Sapiens]. M421 G5 H-U21858 Human **transcriptional activation** 29.15 38.0 kDa factor TAFII32 mRNA, complete cds M424 H3 H-U22662 Human nuclear orphan receptor 49.28 49.0 kDa LXR-alpha mRNA, complete cds M271 D2 H-U24074 killer cell inhibitory receptor 37.62 43 [KIR], Homo sapiens natural killer-associated transcript 3 (NKAT3), complete cds. RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES. 169-29 H-U24153 human p21-activated protein 60 57.82 kinase (Pak2) gene M385 H2 H-U24166 EB1 29.59 36.0 kDa G1 H-U24169 Human JTV-1 (JTV-1) mRNA, 34.43 40 complete cds E1 H-U24576 Human breast tumor autoantigen 18.26 27 mRNA, complete sequence G4 H-U24577 Human LDL-phospholipase A2 48.62 52 mRNA, complete cds H1 H-U25789 Human ribosomal protein L21 17.71 32 mRNA, complete cds M416 D1 H-U25849 Human red cell-type low 17.49 28.0 kDa molecular weight acid phosphatase (ACP1) gene, 5' flanking region and M300 A3 H-U26312 heterochromatin protein H-P1Hs- 19.14 30 gamma M416 D3 H-U26403 Human receptor

PGPUB-DOCUMENT-NUMBER: 20030072794

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030072794 A1

TITLE: Encapsulation of plasmid DNA (lipogenes.TM.) and therapeutic agents with nuclear localization signal/fusogenic peptide conjugates into targeted liposome complexes

PUBLICATION-DATE: April 17, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Boulikas, Teni	Mountain View	CA	US	

APPL-NO: 09/ 876904

DATE FILED: June 8, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60210925 20000609 US

US-CL-CURRENT: 424/450, 264/4 , 435/320.1 , 435/458 , 514/44

ABSTRACT:

A method is disclosed for encapsulating plasmids, oligonucleotides or negatively-charged drugs into liposomes having a different lipid composition between their inner and outer membrane bilayers and able to reach primary tumors and their metastases after intravenous injection to animals and humans. The formulation method includes complex formation between DNA with cationic lipid molecules and fusogenic/NLS peptide conjugates composed of a hydrophobic chain of about 10-20 amino acids and also containing four or more histidine residues or NLS at their one end. The encapsulated molecules display therapeutic efficacy in eradicating a variety of solid human tumors including but not limited to breast carcinoma and prostate carcinoma. Combination of the plasmids, oligonucleotides or negatively-charged drugs with other anti-neoplastic drugs (the positively-charged cis-platin, doxorubicin) encapsulated into liposomes are of therapeutic value. Also of therapeutic value in cancer eradication are combinations of encapsulated the plasmids, oligonucleotides or negatively-charged drugs with HSV-tk plus encapsulated ganciclovir.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority under 35 U.S.C. .sctn.119(e) to U.S. Provisional Application Serial No. 60/210,925 filed Jun. 9, 2000. The contents of this application is hereby incorporated by reference into the

present disclosure.

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Detail Description Table CWU - DETL (5):
KRRKHP (SEQ ID NO:66) found to be efficient NLS. The last two are less effective NLS, KYRKHP (SEQ ID NO:67) resulting in both nuclear and cytoplasmic location of .beta.-galactosidase KHRRHP (SEQ ID NO:68) fusion protein. KHKKHP (SEQ ID NO:69) RHLKHP (SEQ ID NO:70) KHRKYP (SEQ ID NO:71) KHRQHP (SEQ ID NO:72) PETTVVRRRGRSPRRRTPSP Double NLS of hepatitis B virus core antigen. The two underlined RRRRSPRRRRSQS (SEQ ID arginine clusters represent distinct and independent NLS. Mutagenesis NO:73) showed that the antigen fails to accumulate in the nucleus only when (One sequence, C-terminus) both NLS are simultaneously deleted or mutated. ASKSRKRKL Viral Jun, a transcription factor of the AP-1 complex. Accumulates in (SEQ ID NO:74) nuclei most rapidly during G2 and slowly during G1 and S. The cell cycle dependence of viral but not of cellular Jun is due to a C.fwdarw.S mutation in NLS of viral Jun. This NLS conjugated to rabbit IgG can mediate cell cycle-dependent translocation. GGLCSARLHRHALLAT Human T-cell leukemia virus Tax trans-activator protein. The most (SEQ ID NO:75) basic region within the 48 N-terminal segment. Missense mutations in this domain result in its cytoplasmic retention. DTREKKKFLKRRLLRLDE Mouse nuclear Mx1 protein (72 kD), Induced by interferons (among (604-620) 20 other proteins) . Selectively inhibits influenza virus mRNA (SEQ ID NO:76) synthesis in the nucleus and virus multiplication. The cytoplasmic Mx2 has R.fwdarw.S and R.fwdarw.E changes in this region. CGYGPKKKRKV (SV40 large Synthetic peptides crosslinked to bovine serum albumin (BSA) and T) (SEQ ID NO:77) introduced into MCF 7 or HeLa S3 cells with viral co-internalization CGYGDRNKKKKE (human method using adenovirus serotype 3B induced nuclear import of BSA. retinoic acid receptor) (SEQ ID NO:78) CGYGARKTKKKIK (human **glucocorticoid receptor**) (SEQ ID NO:79) CGYGIRKDRRGGR (human estrogen receptor) (SEQ ID NO:80) CGYGARKLKKLGN (human androgen receptor) (SEQ ID NO:81) RKRQRALMLRQAR Human XPAC (xeroderma pigmentosum group A complementing 30-42 protein) involved in DNA excision repair. By site-directed (SEQ ID NO:82) mutagenesis and immunofluorescence. NLS is encoded by exon 1 which is not essential for DNA repair function. EYLSRKGKLEL (SEQ ID T-DNA-linked VirD2 endonuclease of the Agrobacterium NO:83) tumefaciens tumor-inducing (T.sub.i) plasmid. A fusion protein with .beta.- (at the N-terminus) galactosidase is targeted to the nucleus. The T-plasmid integrates into plant nuclear DNA; VirD2 produces a site-specific nick for T integration. VirD2 also contains a bipartite NLS at its C-terminus (see Table 2). KKSKKKRC (SEQ ID NO:84) Putative core NLS of yeast TRM1 (63 kD) that encodes the tRNA (95-102) modification enzyme N.sup.2, N.sup.2-dimethylguanosine-specific tRNA **methyltransferase.** Localizes at the nuclear periphery. The 70-213 amino acid segment of TRM1 causes nuclear localization of .beta.- galactosidase fusion protein in yeast cells. Site-directed mutagenesis of the 95-102 peptide resulted in its cytoplasmic retention. TRM1 is both nuclear and mitochondrial. The 1-48 amino acid segment specifies mitochondrial import. PQSRKKLR (SEQ ID NO:85) Max protein; specifically interacts with c-Myc protein. Fusion of 126- 151 segment of Max to chicken pyruvate kinase (PK) gene, including this putative NLS, followed by transfection of COS-1 cells and indirect immunofluorescence with anti-PK

showed nuclear targeting. QPQRYGGGRGRRW (SEQ ID Gag protein of human foamy retrovirus; a mutant that completely lacks NO:86) this box exhibits very little nuclear localization; binds DNA and RNA in vitro.

PGPUB-DOCUMENT-NUMBER: 20030068675

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030068675 A1

TITLE: Position dependent recognition of GNN nucleotide triplets by zinc fingers

PUBLICATION-DATE: April 10, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Liu, Qiang	Foster City	CA	US	

APPL-NO: 09/ 990186

DATE FILED: November 20, 2001

RELATED-US-APPL-DATA:

child 09990186 A1 20011120

parent continuation-in-part-of 09535008 20000323 US PENDING

child 09990186 A1 20011120

parent continuation-in-part-of 09716637 20001120 US PENDING

non-provisional-of-provisional 60126238 19990324 US

non-provisional-of-provisional 60126239 19990324 US

non-provisional-of-provisional 60146595 19990730 US

non-provisional-of-provisional 60146615 19990730 US

US-CL-CURRENT: 435/69.1, 435/226 , 435/6 , 702/19

ABSTRACT:

The specificity of binding of a zinc finger to a triplet or quadruplet nucleotide target subsite depends upon the location of the zinc finger in a multifinger protein and, hence, upon the location of its target subsite within a larger target sequence. The present disclosure provides zinc finger amino acid sequences for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite, that have been optimized with respect to the location of the subsite within the target site. Accordingly, the disclosure provides finger position-specific amino acid sequences for the recognition of GNN target subsites. This allows the construction of multi-finger zinc finger proteins with improved affinity and specificity for

their target sequences, as well as enhanced biological activity.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] The present application is a continuation-in-part of copending U.S. patent application Ser. No. 09/535,008, filed Mar. 23, 2000, which application claims the benefit of U.S. provisional applications No. 60/126,238, filed Mar. 24, 1999, No. 60/126,239 filed Mar. 24, 1999, No. 60/146,595 filed Jul. 30, 1999 and No. 60/146,615 filed Jul. 30, 1999. The present application is also a continuation-in-part of copending U.S. patent application Ser. No. 09/716,637, filed Nov. 20, 2000. The disclosures of all of the aforementioned applications are hereby incorporated by reference in their entireties for all purposes.

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Brief Description of Drawings Paragraph - DRTX (40):

[0056] Zinc finger proteins are often expressed with a heterologous domain as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcription factor domains (activators,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for represssing expression of a target gene is a KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J. Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell. Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J. Virol. 72:5610-5618 (1998) and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

PGPUB-DOCUMENT-NUMBER: 20030065157

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030065157 A1

TITLE: Genes expressed in lung cancer

PUBLICATION-DATE: April 3, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Lasek, Amy W.	Oakland	CA	US	

APPL-NO: 10/ 116802

DATE FILED: April 4, 2002

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60281593 20010404 US

US-CL-CURRENT: 536/23.1

ABSTRACT:

The present invention relates to a combination comprising a plurality of cDNAs which are differentially expressed in a respiratory disorder and which may be used in their entirety or in part to diagnose, to stage, to treat, or to monitor the treatment of a subject with a respiratory disorder.

[0001] This application claims benefit of provisional application 60/281,593, filed 4 Apr. 2001.

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Detail Description Table CWU - DETL (8):
322 1362715CB1 1816113 g6457338 1.00E-69 E2IG1 [Homo sapiens] 323 3117642CB1 3117642 g3300092 4.00E-69 prostate associated PAGE-1 [Homo sapiens] 324 2026270CB1 2026270 g190726 9.00E-68 parathyroid hormone-related protein precursor [Homo sapiens] 325 981662.2 4401727 g7022306 3.00E-67 unnamed protein product [Homo sapiens] 326 453004.10 2394888 g4704752 6.00E-67 calpain 3; calcium activated neutral protease; CAPN3; CL1 [Homo sapiens] 327 978147.7 2784394 g7022973 5.00E-66 unnamed protein product [Homo sapiens] 328 2132626CB1 541875 g3171914 6.00E-66 RAMP3 [Homo sapiens] 329 402716.37 4199466 g3582143 1.00E-65 DNA-binding zinc finger(GBF) [Homo sapiens] 330 464482.1 625374 g181227 3.00E-65 cytochrome b5 [Homo sapiens] 331 402716.20 4199466 g2745961 1.00E-64 Bcd orf2 [Homo sapiens] 332 1137710.5 1713191 g471126 4.00E-64 Id-2H [Homo sapiens] 333 348912.3 1716655 g219936 2.00E-62

NCA-W272 [Homo sapiens] 334 474926.11 2512203 g312334 1.00E-61 macrophage migration inhibitory factor [Homo sapiens] 335 406804.4 3130454 g6331328 1.00E-61 KIAA1280 protein [Homo sapiens] 336 480855.1 3234063 g6808254 1.00E-60 hypothetical protein [Homo sapiens] 337 238593.5 211779 g7106770 3.00E-60 HSPC190 [Homo sapiens] 338 373514.7 4740251 g8515711 3.00E-60 EXP35 [Homo sapiens] 339 1383354.10 5057204 g6983729 4.00E-60 dJ977B1.5 (myosin regulatory light chain 2, smooth muscle isoform) [Homo sapiens] 340 3120070CB1 3120070 g7582391 4.00E-57 p53 apoptosis-associated target [Mus musculus] 341 253987.19 2232658 g395338 2.00E-55 helix-loop-helix protein [Homo sapiens] 342 133425.16 3510656 g178349 2.00E-54 fructose 1,6-bisphosphatase (EC 3.1.3.11) [Homo sapiens] 343 468221.18 1662856 g1469920 5.00E-54 D53 [Homo sapiens] 344 020093.8 2102756 g573114 6.00E-54 Clq B-chain precursor [Homo sapiens] 345 1556751CB1 1986121 g7959303 1.00E-52 KIAA1518 protein [Homo sapiens] 346 1397976.1 4628258 g306799 2.00E-52 pregnancy-specific beta-glycoprotein e [Homo sapiens] 347 233828.16 1362831 g7021111 2.00E-52 unnamed protein Product [Homo sapiens] 348 1253414CB1 5681633 g450281 6.00E-52 isolog of yeast sui1 and rice gos2; putative [Homo sapiens] 349 1101068.1 5856402 g6164743 4.00E-51 F-box protein Fbx20 [Homo sapiens] 350 006922.1 2934515 g7242957 4.00E-49 KIAA 1301 protein [Homo sapiens] 351 333398.5 2456903 g6502523 2.00E-48 Smad6 protein [Homo sapiens] 352 235725.21 2095728 g2407068 3.00E-48 TFAR19 [Homo sapiens] 353 242472.14 4572916 g34416 1.00E-47 precursor (AA -19 to 692) [Homo sapiens] 354 253550.20 3397390 g183116 3.00E-46 insulin-like growth factor-binding protein [Homo sapiens] 355 216262.3 3813934 g4128051 5.00E-46 EBI1-31 ligand chemokine [Homo sapiens] 356 235191.3 1997915 g6706799 5.00E-46 dJ447F3.2 (ubiquitin-conjugating enzyme E2 H10) [Homo sapiens] 357 480337.45 4602215 g1167 4.00E-45 cpn10 protein [Bos taurus] 358 199939.6 1858415 g2232019 8.00E-44 HPV16 E1 protein binding protein [Homo sapiens] 359 201204.9 4088394 g4323528 1.00E-43 cell cycle protein CDC20 [Homo sapiens] 360 201887.2 3478024 g2988398 2.00E-43 Unknown gene product [Homo sapiens] 361 1136056.1 3527982 g1082038 3.00E-43 G053 is human homolog of mouse FOSB gene [Homo sapiens] 362 994977.1 3722056 g30102 4.00E-43 type I collagen [Homo sapiens] 363 888669.8 4721466 g7329217 6.00E-42 TS58 [Homo sapiens] 364 345860.20 5160686 g29710 9.00E-42 preprocathepsin H (AA -22 to 314) [Homo sapiens] 365 480337.43 1459082 g6996446 2.00E-39 chaperonin 10, Hsp10 protein [Homo sapiens] 365 480337.43 4602215 g6996446 2.00E-39 chaperonin 10, Hsp10 protein [Homo sapiens] 366 399300.14 2842978 g3818590 2.00E-38 alpha-catenin-like protein; CG-4 [Homo sapiens] 367 368015.2 3115792 g7717449 3.00E-38 Homo sapiens chromosome 21 segment HS21C103. 368 227550.1 3771020 g4028563 7.00E-38 brain and nasopharyngeal carcinoma susceptibility protein NSG-x [Homo sapiens] 369 201906.6 3733666 g7416858 2.00E-36 MBIP [Homo sapiens] 370 349589.10 127321 g2370126 6.00E-36 LIM-31 domain protein [Homo sapiens] 371 3713867CB1 2061401 g28608 4.00E-35 precursor polypeptide (AA -36 to 479) [Homo sapiens] 372 235943.27 2957567 g188870 1.00E-34 polymorphic epithelial mucin [Homo sapiens] 373 241742.1 1295905 g190168 2.00E-34 Homo sapiens dinucleotide repeat polymorphism, at locus D5S178 374 333680.1 3138456 g7295285 4.00E-34 melt gene product [Drosophila melanogaster] 375 411429.3 1424886 g4929719 9.00E-34 CGI-125 protein [Homo sapiens] 376 2356055CB1 2356055 g6580815 9.00E-34 indolethylamine N-**methyltransferase** [Homo sapiens] 377 239579.3 1704713 g3462455 2.00E-33 junctional adhesion molecule [Mus musculus] 378 332240.1 2201507 g7022637 3.00E-32 unnamed protein product [Homo sapiens] 379 255161.1 2270986 g7107421 3.00E-32 ferritin light chain [Cavia porcellus] 380 2454384CB1 2454384 g1293145 2.00E-31 rhotekin [Mus

musculus] 381 1383298.3 1510539 g1711117 6.00E-31 ligand **activated transcription** factor PPARgamma2 [Homo sapiens] 382 383376.7 5551761 g340361 1.00E-30 von Willebrand factor prepropeptide [Homo sapiens] 383 230816.1 1526322 g7340847 2.00E-29 chondroitin 4-sulfotransferase [Mus musculus] 384 211949.2 1966295 g5817053 3.00E-29 hypothetical protein [Homo sapiens] 385 238853.42 1450886 g386803 2.00E-28 40-kDa keratin protein [Homo sapiens] 386 333165.2 1682337 g7020625 6.00E-28 unnamed protein product [Homo sapiens] 387 344868.12 3333118 g4761222 1.00E-27 Homo sapiens NADP+-dependent isocitrate dehydrogenase (PICD) mRNA, complete cds. 388 148304.14 3646303 g8131858 1.00E-27 putative thymic stromal co-transporter TSCOT [Mus musculus] 389 247747.6 3124204 g4377993 6.00E-27 tumor transforming protein 1 [Homo sapiens] 390 001153.12 5546984 g505033 4.00E-26 mitogen inducible gene mig-2 [Homo sapiens] 391 1095728.19 414480 g7209525 1.00E-25 DRAL/Slim3/FHL2 [Homo sapiens] 392 222604.7 2745735 g7293742 4.00E-25 CG15881 gene product [Drosophila melanogaster] 393 1094984.14 2620487 g6330840 9.00E-25 KIAA1247 protein [Homo sapiens] 394 400702.1 1969974 g7770167 9.00E-25 PRO2176 [Homo sapiens] 395 196557.1 1927026 g2570154 3.00E-24 17-kDa PKC-potentiated inhibitory protein of PP1 [Sus scrofa] 396 237208.5 993365 g8037909 6.00E-24

PGPUB-DOCUMENT-NUMBER: 20030064395

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030064395 A1

TITLE: Methods for detecting intermolecular interactions in vivo and in vitro

PUBLICATION-DATE: April 3, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Chung, Jay H.	Bethesda	MD	US	

APPL-NO: 10/ 191949

DATE FILED: July 8, 2002

RELATED-US-APPL-DATA:

child 10191949 A1 20020708

parent continuation-of 09054281 19980402 US GRANTED

parent-patent 6444421 US

non-provisional-of-provisional 60080234 19970403 US

US-CL-CURRENT: 435/6, 435/455 , 435/91.2

ABSTRACT:

Methods for assessing intermolecular interactions in vivo and in vitro are provided. Methods are provided for detecting protein-DNA interactions in vivo, in which a cell having a chimeric guide endonuclease molecule and a target nucleic acid is provided, and cleavage of the target nucleic acid by the chimeric guide endonuclease molecule is monitored. Cleavage by the chimeric guide molecule corresponds to binding of the guide domain to the target nucleic acid, or to a protein associated with the nucleic acid. The methods of the invention are adapted to cleavage of target nucleic acids, amplification of target nucleic acids, detection of target nucleic acids, screening of genomic target nucleic acid sequences for guide binding domains, and screening for modulators of chimeric guide binding domain activity. Also provided are methods for detecting interactions between other molecules, including hormones and receptors, enzymes and substrates, and the like.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. patent application Ser. No. 08/826,622, filed Apr. 3, 1997, which was converted to provisional application

Ser. No. _____ by way of petition filed on Nov. 19, 1997. This application is also related to co-filed U.S. patent application by Jay Chung entitled "Chimeric Endonucleases for Detecting Protein-nucleic Acid Interaction In Vivo and In Vitro," filed Apr. 3, 1997, Ser. No. 08/825,664, which was converted to provisional application Ser No._____ by way of petition filed on Nov. 19, 1997, and to co-filed patent application Ser. No. _____ by Jay Chung entitled "Chimeric Endonucleases For Detecting Intermolecular Interactions In Vivo And In Vitro", filed on Apr. 2, 1998 as Attorney Docket No. 15280-31820US. These applications are incorporated by reference in their entireties for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (96):

[0118] Common guide domains include **transcription factors (activators), silencers, nuclear receptors, general transcription** machinery and modifiers of these factors, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.), tumor promoters, metastasis and invasiveness promoters or suppressors and their associated factors and modifiers; tumor suppressors (e.g. p53, WT1, MDM2, Rb family) and their associated factors and modifiers; DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers, cell cycle proteins and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases) and their associated factors and modifiers; RNA modifying enzymes and their associated factors and modifiers, RNA binding factors (directly or indirectly) and their associated factors and modifiers, factors that control chromatin, DNA, RNA and RNP (ribonuclear protein) structure, movement and localization and their associated factors and modifiers; factors derived from microbes (e.g., prokaryotes, eukaryotes and virus) and factors that associate with or modify them.

PGPUB-DOCUMENT-NUMBER: 20030054515

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030054515 A1

TITLE: Protein-protein interactions

PUBLICATION-DATE: March 20, 2003

INVENTOR-INFORMATION:

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Heichman, Karen	Salt Lake City	UT	US	
Bartel, Paul L.	Salt Lake City	UT	US	

APPL-NO: 10/ 024595

DATE FILED: December 21, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60256982 20001221 US

US-CL-CURRENT: 435/183, 435/6 , 435/7.1 , 530/388.26

ABSTRACT:

The present invention relates to the discovery of novel protein-protein interactions that are involved in mammalian physiological pathways, including physiological disorders or diseases. Examples of physiological disorders and diseases include non-insulin dependent diabetes mellitus (NIDDM), neurodegenerative disorders, such as Alzheimer's Disease (AD), and the like. Thus, the present invention is directed to complexes of these proteins and/or their fragments, antibodies to the complexes, diagnosis of physiological generative disorders (including diagnosis of a predisposition to and diagnosis of the existence of the disorder), drug screening for agents which modulate the interaction of proteins described herein, and identification of additional proteins in the pathway common to the proteins described herein.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is related to U.S. provisional patent application Serial No. 60/256,982, filed on Dec. 21, 2000, incorporated herein by reference, and claims priority thereto under 35 USC .sctn.119(e).

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (37):

[0035] The final kinase-related NCOA2 interactor is the novel protein PN12361. PN12361 is similar to the protein product of the mouse AZ2 gene (GenBank accession AB007141). AZ2 is induced upon exposure 5-azacytidine, an inhibitor of DNA **methyltransferase** (Miyagawa et al., 1999). The AZ2 protein is primarily cytoplasmic and is found in the testis, brain and lung of mouse. The amino-terminus of the AZ2 protein is similar to ITRAF and TBK1, two proteins involved in the kinase-dependent signal transduction cascade leading to NFkappaB activation. In fact, overexpression of AZ2 has been shown to inhibit TNF alpha-mediated activation of NFkappaB. Taken together, the finding that NCOA2 and the novel AZ2-like protein PN12361 can interact suggests that NCOA2 maybe capable of influencing the **activation of other transcriptional** regulators such as NFkappaB.

PGPUB-DOCUMENT-NUMBER: 20030049649

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030049649 A1

TITLE: Targeted modification of chromatin structure

PUBLICATION-DATE: March 13, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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Collingwood, Trevor			US	
Snowden, Andrew			US	

APPL-NO: 10/ 084826

DATE FILED: February 24, 2002

RELATED-US-APPL-DATA:

child 10084826 A1 20020224

parent continuation-in-part-of 09844508 20010427 US PENDING

non-provisional-of-provisional 60200590 20000428 US

non-provisional-of-provisional 60228523 20000828 US

US-CL-CURRENT: 435/6, 435/199 , 435/455 , 435/468

ABSTRACT:

Methods and compositions for targeted modification of chromatin structure, within a region of interest in cellular chromatin, are provided. Such methods and compositions are useful for facilitating processes such as, for example, transcription and recombination, that require access of exogenous molecules to chromosomal DNA sequences.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of copending U.S. patent application Ser. No. 09/844,508 (filed Apr. 27, 2001), which in turn claims priority to U.S. Provisional Patent Application Serial No. 60/200,590, filed Apr. 28, 2000 and to U.S. Provisional Patent Application Serial No. 60/228,523, filed Aug. 28, 2000. The disclosures of all of the aforementioned patent applications are hereby incorporated by reference in their entireties.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (9):

[0008] A number of enzymes capable of chemical modification of histones have been described and partially characterized. For example, histone acetyl transferases include Gcn5p, p300/CBP-associated factor (P/CAF), p300, CREB-binding protein (CBP), HAT1, TFIID-associated factor 250 (TAF.sub.II250), and **steroid receptor** coactivator-1 (SRC-1). Wade et al. (1997) Trends Biochem. Sci. 22:128-132; Kouzarides (1999) Curr. Opin. Genet. Devel. 9:40-48; Sterner et al. (2000) Microbiol. Mol. Biol. Rev. 64:435-459. The HDAC family of proteins have been identified as histone deacetylases and include homologues to the budding yeast histone deacetylase RPD3 (e.g., HDAC1, HDAC2, HDAC3 and HDAC8) and homologues to the budding yeast histone deacetylase HDA1 (e.g., HDAC4, HDAC5, HDAC6 and HDAC7). Ng et al. (2000) Trends Biochem. Sci. 25:121-126. The Rsk-2 (RKS90) kinase has been identified as a histone kinase. Sassone-Corsi et al. (1999) Science 285:886-891. A histone **methyltransferase** (CARM-1) has also been identified. Chen et al. (1999) Science 284:2174-2177.

PGPUB-DOCUMENT-NUMBER: 20030049623

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030049623 A1

TITLE: PR/SET-domain containing nucleic acids, polypeptides, antibodies and methods of use

PUBLICATION-DATE: March 13, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Huang, Shi	San Diego	CA	US	

APPL-NO: 09/ 910478

DATE FILED: July 18, 2001

US-CL-CURRENT: 435/6, 435/320.1 , 435/325 , 435/455 , 435/69.1 , 530/350 , 536/23.2

ABSTRACT:

The present invention provides an isolated nucleic acid molecule encoding a PFM/SET polypeptide. Also provided is an isolated nucleic acid molecule encoding a functional fragment of a PFM/SET polypeptide that contains a PR, SET, PRAZ or PKZL domain of a PFM/SET polypeptide of the invention. Further provided by the invention are PFM/SET polypeptides, and functional fragments thereof that contain a PR, SET, PRAZ or PKZL domain of a PFM/SET polypeptide. The invention also provides PFM/SET antibodies, PFM/SET modulatory compounds, and related methods. The molecules and methods of the invention can be used to modulate cell proliferation to prevent or treat proliferative disorders, including cancer. Additionally, the molecules and methods of the invention can be used to diagnose and prognose proliferative disorders.

---------- KWIC ---------

Detail Description Paragraph - DETX (121):

[0149] The methods of the invention for identifying a PFM/SET modulatory compound can involve determining an activity of PFM/SET. Exemplary activities include, for example, transcriptional activity and **methyltransferase** activity (see, for example, Huang et al., J. Biol. Chem. 273:15933-15939 (1998). Suitable assays for identifying compounds that modulate PFM/SET **transcriptional activation,** repression and coactivation function can be determined by the skilled person. Such assays are generally based on co-expression of PFM/SET and an appropriate promoter-linked reporter gene in a cell, under conditions where a certain amount of transcription occurs, contacting the cell with the candidate compound, and determining whether there is a change (i.e. either an

increase or decrease) in transcriptional activity. Transcription based assays are well known in the art, and readily amenable to high-throughput screening assays.

PGPUB-DOCUMENT-NUMBER: 20030046722

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030046722 A1

TITLE: Methods for cloning mammals using reprogrammed donor chromatin or donor cells

PUBLICATION-DATE: March 6, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 10/ 032191

DATE FILED: December 21, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60258151 20001222 US

US-CL-CURRENT: 800/21

ABSTRACT:

The invention provides methods for cloning mammals that allow the donor chromosomes or donor cells to be reprogrammed prior to insertion into an enucleated oocyte. The invention also features methods of inserting chromosomes or nuclei into recipient cells.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (13):

[0011] In preferred embodiments of any of the above aspects, the reprogramming media (e.g., a cell extract) is modified by the enrichment or depletion of a factor, such as a DNA **methyltransferase,** histone deacetylase, histone, protamine, nuclear lamin, **transcription factor, activator,** or repressor. In other preferred embodiments, the level of expression of NuMA or AKAP95 protein in the oocyte or chimeric embryo is at least 2, 5, 10, or 20-fold greater in the nucleus than in the cytoplasm. In yet other embodiments, at least 30, 40, 50, 60, 70, 80, 90, or 100% of the AKAP95 protein in the oocyte or chimeric embryo is extracted with a solution of 0.1% Triton X-100, 1 mg/ml DNase I, and either 100 mM or 300 mM NaCl. Preferably, the chromatin mass is purified from the reprogramming media (e.g., extract) prior

to insertion into the enucleated oocyte. In another preferred embodiment, inserting the chromatin mass into the enucleated oocyte involves contacting the chromatin mass and the oocyte with a fusigenic compound under conditions that allow the chromatin mass to enter the ooctye. In yet another preferred embodiment, the fetus develops into a viable offspring. Preferably, at least 1, 3, 5, 10, 20, 30, 40, 50, 60, 70, 80, or 90% of the nuclear transfer oocytes or embryos develop into viable offspring. In this method, the oocyte containing the chromatin mass or reprogrammed cell may be cultured under conditions that allow cell division and one of the resulting cells may be recloned one or more times. The donor nucleus, donor chromatin mass, or donor cell and the oocyte used in the method may be from the same species, or they may be from different species or genuses. The mammal may be a human or non-human mammal, and the oocyte may be fertilized or unfertilized. Preferably the donor nucleus, chromatin mass, or permeabilized cell is from a G.sub.1 or G.sub.0 phase cell. In addition, the genomic DNA of the cloned embryo, fetus, or mammal is preferably substantially identical to that of the donor cell. It is also contemplated that the chromatin mass or reprogrammed cell may be inserted into an embryo for the production of a chimeric embryo, fetus, or mammal containing a mixture of cells with DNA substantially identical to that of the chromatin mass or reprogrammed cell and cells with DNA substantially identical to that of the naturally-occurring cells in the embryo. It is also contemplated that a nucleated oocyte may be used in the methods of the invention.

Summary of Invention Paragraph - BSTX (32):

[0030] Exemplary reprogramming media include solutions, such as buffers, that do not contain biological molecules such as proteins or nucleic acids. Such solutions are useful for the removal of one or more factors from a nucleus, chromatin mass, or chromosome. Other preferred reprogramming medias are extracts, such as cellular extracts from cell nuclei, cell cytoplasm, or a combination thereof. Exemplary cell extracts include extracts from oocytes (e.g., mammalian, vertebrate, or invertebrate oocytes), male germ cells (mammalian, vertebrate, or invertebrate germ cells such as spermatogonia, spermatocyte, spermatid, or sperm), and stem cells (e.g., adult or embryonic stem cells). Yet other reprogramming media are solutions or extracts to which one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, protamines, nuclear lamins, **transcription factors, activators,** repressors, chromatin remodeling proteins, growth factors, interleukins, cytokines, or other hormones) have been added, or extracts from which one or more factors have been removed. Still other reprogramming media include solutions of detergent (e.g., 0.01% to 0. 1%, 0. 1% to 0.5%, or 0.5% to 2% ionic or non-ionic detergent such as one or more of the following detergents: SDS, Triton X-100, Triton X-114, CHAPS, Na-deoxycholate, n-octyl glucoside, Nonidet P40, IGEPAL, Tween 20, Tween 40, or Tween 80), salt (e.g., .about.0.1, 0.15, 0.25, 0.5, 0.75, 1, 1.5, or 2 M NaCl or KCl), polyamine (e.g., .about.1 .mu.M, 10 .mu.M, 100 .mu.M, 1 mM or 10 mM spermine, spermidine, protamine, or poly-L-lysine), a protein kinase (e.g., cyclin-dependent kinase 1, protein kinase C, protein kinase A, MAP kinase, calcium/calmodulin-dependent kinase, CK1 casein kinase, or CK2 casein kinase), and/or a phosphatase inhibitor (e.g., .about.10 .mu.M, 100 .mu.M, 1 mM, 10 mM, 50 mM, 100 mM of one or more of the following inhibitors: Na-orthovanadate, Na-pyrophosphate, Na-fluoride, NIPPI,

inhibitor 2, PNUTS, SDS22, AKAP149, or ocadaic acid). In some embodiments, the reprogramming medium contains an anti-NuMA antibody. If desired, multiple reprogramming media may be used simultaneously or sequentially to reprogram a donor cell, nucleus, or chromatin mass.

Summary of Invention Paragraph - BSTX (38):

[0036] By "enrichment or depletion of a factor" is meant the addition or removal of a naturally-occurring or recombinant factor by at least 20, 40, 60, 80, or 100% of the amount of the factor originally present in an reprogramming media (e.g., a cell extract). Alternatively, a naturally-occurring or recombinant factor that is not naturally present in the reprogramming media may be added. Preferred factors include proteins such as DNA **methyltransferases,** histone deacetylases, histones, protamines, nuclear lamins, **transcription factors, activators,** and repressors; membrane vesicles, and organelles. In one preferred embodiment, the factor is purified prior to being added to the reprogramming media, as described below. Alternatively, one of the purification methods described below may be used to remove an undesired factor from the reprogramming media.

Detail Description Paragraph - DETX (7):

[0073] These methods are described further below. It is noted that any of the methods described below can also be performed with reprogramming media other than cell extracts. For example, a reprogramming media can be formed by adding one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, protamines, nuclear lamins, **transcription factors, activators,** repressors, chromatin remodeling proteins, growth factors, interleukins, cytokines, or other hormones) to a solution, such as a buffer. Preferably, one or more of the factors are specific for oocytes or stem cells, such as embryonic stem cells.

Detail Description Paragraph - DETX (41):

[0103] As an alternative to a cell extract, a reprogramming media can also be formed by adding one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, protamines, nuclear lamins, **transcription factors, activators,** repressors, chromatin remodeling proteins, growth factors, interleukins, cytokines, or other hormones) to a solution, such as a buffer. Preferably, one or more of the factors are specific for oocytes or stem cells.

Detail Description Paragraph - DETX (79):

[0139] As an alternative to a cell extract, a reprogramming media can also be formed by adding one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, protamines, nuclear lamins, **transcription factors, activators,** repressors, chromatin remodeling proteins, growth factors, interleukins, cytokines, or other hormones) to a solution, such as a buffer. Preferably, one or more of the factors are specific for oocytes or stem cells.

PGPUB-DOCUMENT-NUMBER: 20030044404

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030044404 A1

TITLE: Regulation of angiogenesis with zinc finger proteins

PUBLICATION-DATE: March 6, 2003

INVENTOR-INFORMATION:

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Liu, Pei-Qi	Richmond	CA	US	
Wolffe, Alan	Orinda	CA	US	
Eisenberg, Stephen P.	Boulder	CO	US	
Jarvis, Eric	Boulder	CO	US	

APPL-NO: 09/ 846033

DATE FILED: April 30, 2001

RELATED-US-APPL-DATA:

child 09846033 A1 20010430

parent continuation-in-part-of 09736083 20001212 US ABANDONED

child 09736083 20001212 US

parent continuation-in-part-of 09733604 20001207 US ABANDONED

US-CL-CURRENT: 424/94.63, 435/226 , 435/320.1 , 435/325 , 435/69.1 , 536/23.2

ABSTRACT:

Provided herein are a variety of methods and compositions for regulating angiogenesis, such methods and compositions being useful in a variety of applications where modulation of vascular formation is useful, including, but not limited to, treatments for ischemia and wound healing. Certain of the methods and compositions accomplish this by using various zinc finger proteins that bind to particular target sites in one or more VEGF genes. Nucleic acids encoding the zinc finger proteins are also disclosed. Methods for modulating the expression of one or more VEGF genes with the zinc finger proteins and nucleic acids are also disclosed. Such methods can also be utilized in a variety of therapeutic applications that involve the regulation of endothelial cell growth. Pharmaceutical compositions including the zinc finger proteins or nucleic acids encoding them are also provided.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. application Ser. No. 09/736,083, filed Dec. 12, 2000, which is a continuation-in-part of U.S. application Ser. No. 09/733,604, filed Dec. 7, 2000, both of which are incorporated herein by reference in their entirety for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (118):

[0212] Zinc finger proteins are often expressed with an exogenous domain (or functional fragment thereof) as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcription factor domains (activators,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for repressing expression of a target gene is a KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J. Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell. Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J. Virol. 72:5610-5618 (1998) and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

PGPUB-DOCUMENT-NUMBER: 20030039980

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030039980 A1

TITLE: Assays for determination of functional binding of compounds to receptors

PUBLICATION-DATE: February 27, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Thompson, John F.	Warwick	RI	US	

APPL-NO: 09/ 967107

DATE FILED: September 28, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60237544 20000930 US

US-CL-CURRENT: 435/6, 435/7.1

ABSTRACT:

The present invention relates to novel processes for determination of functional binding of agents to receptors. The invention provides assays that measure the ligand-dependent interaction between nuclear receptors and nuclear receptor coregulators, including coactivators and corepressors. The invention further provides assays that can measure the ability of test agents to act as effectors of such interactions. The invention also provides pharmaceutical compositions comprising agents identified using the assays of the invention.

CROSSREFERENCE TO RELATED APPLICATION

[0001] This application claims priority from U.S. Provisional Patent Application No. 60/237,544 filed Sep. 30, 2000, the benefit of which is hereby claimed under 37 C.F.R. .sctn.1.78(a)(3).

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (10):

[0009] Nuclear receptor coactivators include **steroid receptor** coactivator-1 (SRC-1), **steroid receptor** coactivator-2 (SRC-2), **steroid receptor coactivator-3 (SRC-3), transcripti n** intermediary factor 2 (TIF2), **glucocorticoid receptor** interacting protein 1 (GRIP1), retinoic acid receptor interacting protein 3 (RAC3), coactivator-associated **arginine methyltransferase** 1 (CARM1), peroxisome

proliferator-activated receptor gamma coactivator-1 (PGC-1), peroxisome proliferator-activated receptor gamma coactivator-2 (PGC-2), p300, CREB binding protein (CBP), p300/CREB-binding protein-interacting protein (p/CIP), p300/CBP-associated factor (P/CAF), nuclear-receptor co-activator (NCoA) proteins, alteration/deficiency in activation (ADA) 3 protein, small nuclear RING finger protein (SNURF), the thyroid hormone receptor-associated proteins (TRAP), and NR-binding SET-domain-containing protein (NSD1).

Summary of Invention Paragraph - BSTX (51):

[0049] In yet another preferred embodiment, the nuclear receptor coregulators provided by the invention include nuclear receptor coactivators. In a more preferred embodiment, the nuclear receptor coactivators provided by the invention include, but are not limited to, **steroid receptor** coactivator-1, **steroid receptor coactivator-2, steroid receptor coactivator-3, transcription** intermediary factor 2, **glucocorticoid receptor** interacting protein 1, retinoic acid receptor interacting protein 3, coactivator-associated **arginine methyltransferase** 1, peroxisome proliferator-activated receptor gamma coactivator-1, peroxisome proliferator-activated receptor gamma coactivator-2, p300/CREB binding protein, p300, CREB-binding protein-interacting protein, nuclear-receptor co-activator protein, p300/CBP-associated factor, alteration/deficiency in activation 3 protein, small nuclear RING finger protein, thyroid hormone receptor-associated protein 220, NR-binding SET-domain-containing protein, any fragment thereof, or any combination thereof.

Detail Description Paragraph - DETX (29):

[0115] In another preferred embodiment, the nuclear receptor coregulator provided by the invention is a nuclear receptor coactivator. In a more preferred embodiment, the nuclear receptor coactivator is chosen from the list comprising a **steroid receptor** coactivator-1 (SRC-1), **steroid receptor** coactivator-2 (SRC-2), **steroid receptor coactivator-3 (SRC-3), transcription** intermediary factor 2 (TIF2), **glucocorticoid receptor** interacting protein 1 (GRIP1), retinoic acid receptor interacting protein 3 (RAC3), coactivator-associated **arginine methyltransferase** 1 (CARM1), peroxisome proliferator-activated receptor gamma coactivator-1 (PGC-1), peroxisome proliferator-activated receptor gamma coactivator-2 (PGC-2), p300, CREB binding protein (CBP), p300/CREB-binding protein-interacting protein (p/CIP), nuclear-receptor co-activator (NCoA) proteins, p300/CBP-associated factor (P/CAF), alteration/deficiency in activation (ADA) 3 protein, small nuclear RING finger protein (SNURF), the thyroid hormone receptor-associated proteins (TRAP), NR-binding SET-domain-containing protein (NSD1), any fragment thereof and any combination thereof.

Claims Text - CLTX (13):

12. The method as defined in claim 11 wherein said nuclear receptor coactivator is a **steroid receptor** coactivator-1, **steroid receptor coactivator-2, steroid receptor coactivator-3, transcription** intermediary factor 2, **glucocorticoid receptor** interacting protein 1, retinoic acid receptor interacting protein 3, coactivator-associated **arginine methyltransferase** 1,

peroxisome proliferator-activated receptor gamma coactivator-1, peroxisome proliferator-activated receptor gamma coactivator-2, p300/CREB binding protein, p300, CREB-binding protein-interacting protein, nuclear-receptor co-activator protein, p300/CBP-associated factor, alteration/deficiency in activation 3 protein, small nuclear RING finger protein, thyroid hormone receptor-associated protein 220, NR-binding SET-domain-containing protein, any fragment thereof, or any combination thereof.

Claims Text - CLTX (34):

33. The method as defined in claim 32 wherein said nuclear receptor coactivator is **steroid receptor** coactivator-1, **steroid receptor coactivator-2, steroid receptor coactivator-3, transcription** intermediary factor 2, **glucocorticoid receptor** interacting protein 1, retinoic acid receptor interacting protein 3, coactivator-associated **arginine methyltransferase** 1, peroxisome proliferator-activated receptor gamma coactivator-1, peroxisome proliferator-activated receptor gamma coactivator-2, p300/CREB binding protein, p300, CREB-binding protein-interacting protein, nuclear-receptor co-activator protein, p300/CBP-associated factor, alteration/deficiency in activation 3 protein, small nuclear RING finger protein, thyroid hormone receptor-associated protein 220, NR-binding SET-domain-containing protein, any fragment thereof, or any combination thereof.

PGPUB-DOCUMENT-NUMBER: 20030021776

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030021776 A1

TITLE: Regulation of angiogenesis with zinc finger proteins

PUBLICATION-DATE: January 30, 2003

INVENTOR-INFORMATION:

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Liu, Pei-Qi	Richmond	CA	US	
Wolffe, Alan	Orinda	CA	US	
Eisenberg, Stephen P.	Boulder	CO	US	
Jarvis, Eric	Boulder	CO	US	

APPL-NO: 10/ 006069

DATE FILED: December 6, 2001

RELATED-US-APPL-DATA:

child 10006069 A1 20011206

parent continuation-in-part-of 09846033 20010430 US PENDING

child 09846033 20010430 US

parent continuation-in-part-of 09736083 20001212 US ABANDONED

child 09736083 20001212 US

parent continuation-in-part-of 09733604 20001207 US ABANDONED

US-CL-CURRENT: 424/94.63, 435/226 , 514/6

ABSTRACT:

Provided herein are a variety of methods and compositions for regulating angiogenesis, such methods and compositions being useful in a variety of applications where modulation of vascular formation is useful, including, but not limited to, treatments for ischemia and wound healing. Certain of the methods and compositions accomplish this by using various zinc finger proteins that bind to particular target sites in one or more VEGF genes. Nucleic acids encoding the zinc finger proteins are also disclosed. Methods for modulating the expression of one or more VEGF genes with the zinc finger proteins and nucleic acids are also disclosed. Such methods can also be utilized in a

variety of therapeutic applications that involve the regulation of endothelial cell growth. Pharmaceutical compositions including the zinc finger proteins or nucleic acids encoding them are also provided.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of copending U.S. application Ser. No. 09/846,033, filed Apr. 30, 2001, which is a continuation-in-part of U.S. application Ser. No. 09/736,083, filed Dec. 12, 2000, which is a continuation-in-part of U.S. application Ser. No. 09/733,604, filed Dec. 7, 2000, all of which are incorporated herein by reference in their entirety for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (122):

[0218] Zinc finger proteins are often expressed with an exogenous domain (or functional fragment thereof) as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcription factor domains (activators,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for repressing expression of a target gene is a KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J. Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell. Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J. Virol. 72:5610-5618 (1998) and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

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TITLE: PRMTs as modifiers of the p53 pathway and methods of use

PUBLICATION-DATE: January 23, 2003

INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/6, 435/15

ABSTRACT:

Human PRMT genes are identified as modulators of the p53 pathway, and thus are therapeutic targets for disorders associated with defective p53 function. Methods for identifying modulators of p53, comprising screening for agents that modulate the activity of PRMT are provided.

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Summary of Invention Paragraph - BSTX (8):
[0006] Coactivator associated **arginine Methyltransferase** 1 (CARM1/PRMT4)

functions in a dual role as a protein **methyltransferase and a transcriptional coactivat r**. CARM1 interacts with the p160 **coactivators t enhance nuclear receptor transcription, enhances transcripti n activation** by the estrogen receptor, and methylates histone H3 (Chen D et al., supra). PRMT6 is the only PRMT capable of automethylation. Of the known PRMTs, CARM1 and PRMT6 localize to the nucleus (Frankel A et al. (2002) J Biol Chem. 277:3537-3543).

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PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020197605 A1

TITLE: Novel Polynucleotides

PUBLICATION-DATE: December 26, 2002

INVENTOR-INFORMATION:

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DATE FILED: December 18, 2000

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COUNTRY	APPL-NO	DOC-ID	APPL-DATE
JP	P. HEI 11-377484	1999JP-P. HEI 11-377484	December 16, 1999
JP	P. 2000-159162	2000JP-P. 2000-159162	April 7, 2000
JP	P. 2000-280988	2000JP-P. 2000-280988	August 3, 2000

US-CL-CURRENT: 435/6, 435/287.2 , 435/91.2

ABSTRACT:

Novel polynucleotides derived from microorganisms belonging to coryneform bacteria and fragments thereof, polypeptides encoded by the polynucleotides and fragments thereof, polynucleotide arrays comprising the polynucleotides and fragments thereof, recording media in which the nucleotide sequences of the polynucleotide and fragments thereof have been recorded which are readable in a computer, and use of them.

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Detail Description Table CWU - DETL (13):
974965 1212 1028 4528 976349 977734 1386 sp:CSP1_CORGL Corynebacterium glutamicum 27.7 56.8 440 major secreted protein PS1 protein (Brevibacterium

flavum) ATCC precursor 17965 csp1 1029 4529 978378 977800 579 gp:SCF56_6 Streptomyces coelicolor A3(2) 44.0 70.0 100 transcriptional regulator (tetR SCF56.06 family) 1030 4530 980740 978368 2373 gp:SCE87_17 Streptomyces coelicolor A3(2) 42.6 70.0 802 membrane transport protein SCE87.17c 1031 4531 980993 981490 498 sp:MENG_HAEIN Haemkophilus influenzae Rd 38.2 75.8 157 S-adenosylmethionine: 2- HI0508 menG demethylmenaquinone **methyltransferase** 1032 4532 981622 982287 666 1033 4533 982674 982294 381 gp:NMA6Z2491_214 Neisseria meningitidis NMA 1953 29.8 63.6 121 hypothetical protein 1034 4534 983100 984650 1551 pir:A70539 Mycobacterium tuberculosis 24.9 48.3 482 hypothetical protein H37Rv Rv1128c 1035 4535 984910 985845 936 1036 4536 986510 984864 1647 pir:I59305 Escherichia coli K12 prfC 39.2 68.0 546 peptide-chain-release factor 3 1037 4537 986739 988007 1269 prf.2406311A Methylophilus methylotrophus 42.8 72.8 404 amide-urea transport protein fmdD 1038 4538 988023 988904 882 prf:2406311B Methylophilus methylotrophus 40.8 61.0 77 amide-urea transport protein fmdE 1039 4539 988904 989980 1077 prf:2406311C Methylophilus methylotrophus 34.6 68.0 234 amide-urea transport protein fmdF 1040 4540 989980 990705 726 sp:BRAF_PSEAE Pseudomonas aeruginosa PAO 37.9 70.0 253 high-affinity branched-chain amino braF acid transport ATP-binding protein 1041 4541 990716 991414 699 sp:BRAG_PSEAE Pseudomonas aeruginosa PAO 35.2 69.1 236 high-affinity branched-chain amino braG acid transport ATP-binding protein 1042 4542 992028 991417 612 sp:PTH_ECOLI Escherichia coli K12 pth 39.0 70.6 187 peptidyl-tRNA hydrolase 1043 4543 992058 993080 1023 sp:2NPD_WILMR Williopsis mrakii IFO 0895 25.2 54.0 361 2-nitropropane dioxygenase 1044 4544 993549 994613 1065 sp:G3P_ZYMMO Streptomyces roseofulvus gap 39.5 72.8 342 glyceraldehyde-3-phosphate dehydrogenase 1045 4545 994474 994106 369 GSP:Y75094 Neisseria meningitidis 54.0 61.0 51 polypeptides predicted to be useful antigens for vaccines and diagnostics 1046 4546 995375 994845 531 sp:PTH_ECOLI Escherichia coli K12 pth 38.5 63.2 174 peptidyl-tRNA hydrolase 1047 4547 996126 995527 600 pir:B70622 Mycobacterium tuberculosis 47.0 65.0 194 50S ribosomal protein L25 H37Rv rplY 1048 4548 996402 996830 429 sp:LGUL_SALTY Salmonella typhimurium D21 28.7 54.6 143 lactoylglutathione lyase gloA 1049 4549 997456 996833 624 prf:2516401BW Bacillus cereus ATCC 10987 38.9 62.5 208 DNA alkylation repair enzyme alkD 1050 4550 998440 997466 975 sp:KPRS_BACCL Bacillus subtilis prs 44.0 79.1 316 ribose-phosphate pyrophosphokinase 1051 4551 999909 998455 1455 pir:S66080 Bacillus subtilis gcaD 42.0 71.9 452 UDP-N-acetylglucosamine pyrophosphorylase 1052 4552 1001242 1000016 1227 1053 4553 1001332 1002864 1533 sp:SUFI_ECOLI Escherichia coli K12 sufI 30.8 61.7 506 sufI protein precursor 1054 4554 1003013 1003930 918 sp:NODI_RHIS3 Rhizobium sp. N33 nodI 35.8 64.8 310 nodulation ATP-binding protein I 1055 4555 1003953 1004783 831 pir:JN0850 Streptomyces lividans ORF2 30.2 63.2 272 hypothetical membrane protein 1056 4556 1004829 1006085 1257 sp:UHPB_ECOLI Escherichia coli K12 uhpB 24.6 48.4 459 two-component system sensor histidine kinase 1057 4557 1006089 1006697 609 prf.2107255A Streptomyces peucetius dnrN 36.6 67.3 202 two component transcriptional regulator (luxR family) 1058 4558 1006937 1006734 204 1059 4559 1006998 1008152 1155 gp:SCF15_7 Streptomyces coelicolor A3(2) 31.5 64.5 349 hypothetical membrane protein SCF15.07 1060 4560 1008622 1010061 1440 pir:S65587 Streptomyces glaucescens strV 28.6 57.0 535 ABC transporter 1061 4561 1008686 1008534 153 1062 4562 1010057 1011790 1734 pir:T14180 Mycobacterium smegmatis exiT 44.0 74.0 573 ABC transporter 1063 4563 1013761 1011797 1965 sp:GGT_ECOLI Escherichia coli K12 ggt 32.4 58.6 666 gamma-glutamyltranspeptidase precursor 1064 4564 1014016 1014264 249 1065 4565 1014861 1014343 519 1066 4566 1014925 1015116 192 1067 4567 1015652

1016560 909 1068 4568 1015692 1015450 243 GPU:AF164956_23 Corynebacterium glutamicum 64.0 72.0 37 transposase protein fragment TnpNC 1069 4569 1015852 1015145 708 gp:AF121000_8 Corynebacterium glutamicum 99.6 100.0 236 transposase (IS1628 TnpB) 22243 R-plasmid pAG1 tnpB 1070 4570 1016557 1017018 462 1071 4571 1017870 1017274 597 1072 4572 1018082 1018393 312 1073 4573 1018416 1019066 651 sp:TETC_ECOLI Escherichia coli tetR 23.0 59.6 183 transcriptional regulator (TetR- family) 1074 4574 1019090 1022716 3627 sp:MFD_ECOLI Escherichia coli mfd 36.2 65.1 1217 transcription/repair-coupling protein 1075 4575 1020613 1019390 1224 1076 4576 1021305 1021078 228 GSP:Y75301 Neisseria gonorrhoeae 48.0 69.0 76 Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics 1077 4577 1024666 1022699 1968 sp:MDLB_ECOLI Escherichia coli mdlB 31.3 62.7 632 multidrug resistance-like ATP- binding protein, ABC-type transport protein 1078 4578 1026396 1024666 1731 sp:YC73_MYCTU Mycobacterium tuberculosis 50.2 81.9 574 ABC transporter H37Rv Rv1273c 1079 4579 1028886 1026505 2382 sp:YLI3_CORGL Corynebacterium glutamicum 100.0 100.0 368 hypothetical membrane protein ATCC 13032 orf3 1080 4580 1031885 1032181 297 1081 4581 1032196 1032780 585 sp.YABN_BACSU Bacillus subtilis yabN 33.4 57.4 183 hypothetical protein 1082 4582 1033185 1032760 426 1083 4583 1033646 1033269 378 1084 4584 1033954 1034739 786 pir:A70623 Mycobacterium tuberculosis 46.5 68.9 241 lpqU protein H37Rv Rv1022 lpqU 1085 4585 1034949 1036223 1275 sp:ENO_BACSU Bacillus subtilis eno 64.5 86.0 422 enolase (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) 1086 4586 1036159 1036016 144 PIR:B72477 Aeropyrum pernix K1 APE2459 68.0 58.0 41 hypothetical protein 1087 4587 1036316 1036855 540 pir:C70623 Mycobacterium tuberculosis 31.9 55.0 191 hypothetical protein H37Rv Rv1024 1088 4588 1036900 1037445 546 pir:D70623 Mycobacterium tuberculosis 59.5 77.8 153 hypothetical protein H37Rv Rv1025 1089 4589 1037448 1038410 963 sp:GPPA_ECOLI Escherichia coli gppA 25.2 55.0 329 guanosine pentaphosphatase or exopolyphosphatase 1090 4590 1037481 1036498 984 1091 4591 1039650 1038721 930 sp:THD2_ECOLI Escherichia coli tdcB 30.3 64.7 314 threonine dehydratase 1092 4592 1039783 1039977 195 1093 4593 1039996 1040325 330 1094 4594 1040494 1040682 189 pir:B72287 Thermotoga maritima MSB8 46.3 74.1 56 hypothetical protein 1095 4595 1040925 1041917 993 sp:RHAR_ECOLI Escherichia coli rhaR 24.8 55.8 242 **transcription activator** of L-rhamnose operon 1096 4596 1042027 1042842 816 pir:F70893 Mycobacterium tuberculosis 57.8 80.1 282 hypothetical protein H37Rv Rv1072 1097 4597 1043236 1042850 387 1098 4598 1043747 1043298 450 gp:SCF55_39 Streptomyces coelicolor A3(2) 30.0 57.1 140 hypothetical protein SCF55.39 1099 4599 1044295 1043774 522 sp:GREA_ECOLI Escherichia coli greA 35.0 60.1 143 transcription elongation factor 1100 4600 1044959 1044477 483 pir:G70894 Mycobacterium tuberculosis 34.3 72.1 140 hypothetical protein H37Rv Rv1081c 1101 4601 1045158 1046030 873 pir:S44952 Streptomyces lincolnensis lmbE 31.7 56.3 300 lincomycin-production 1102 4602 1046073 1046390 318 1103 4603 1046610 1047707 1098 sp:AROG_CORGL Corynebacterium glutamicum 99.2 99.5 367 3-deoxy-D-arabino-heptulosonate-7- aroG phosphate synthase 1104 4604 1047452 1046820 633 1105 4605 1047827 1048501 675 sp:YARF_CORGL Corynebacterium glutamicum 96.0 97.3 97 hypothetical protein or undecaprenyl CCRC18310 pyrophosphate synthetase 1106 4606 1048356 1048529 174 SP:YARF_CORGL Corynebacterium glutamicum 100.0 100.0 28 hypothetical protein (Brevibacterium flavum) 1107 4607 1048525 1049043 519 1108 4608 1049385 1049068 318 1109 4609 1050362 1049427 936 sp:COAA_ECOLI Escherichia coli coaA 53.9 79.9 308 pantothenate kinase 1110 4610 1050624 1051925 1302 gsp:R97745 Brevibacterium flavum MJ-233 99.5 100.0 434 serine hydroxymethyl transferase

glyA 1111 4611 1052021 1053880 1860 sp:PABS_STRGR Streptomyces griseus pabS 47.6 70.1 696 p-aminobenzoic acid synthase 1112 4612 1053880 1054602 723 1113 4613 1054859 1055722 864 1114 4614 1055032 1054640 393 1115 4615 1055783 1056319 537 gp:A01504_1 Alcaligenes faecalis ptcR 30.3 58.8 165 phosphinothricin resistance protin 1116 4616 1057200 1056322 879 sp:YBGK_ECOLI Escherichia coli ybgK 30.3 59.0 300 hypothetical protein 1117 4617 1057573 1058628 1056 1118 4618 1057868 1057200 669 sp:YBGJ_ECOLI Escherichia coli ybgJ 37.8 57.8 225 hypothetical protein 1119 4619 1058598 1057843 756 sp:LAMB_EMENI Emericella nidulans lamB 30.8 52.2 276 lactam utilization protein 1120 4620 1059214 1058624 591 sp:YCSH_BACSU Bacillus subtilis ycsH 40.6 81.2 165 hypothetical membrane protein 1121 4621 1059218 1059889 672 1122 4622 1059360 1059962 603 1123 4623 1060112 1060792 681 sp:YDHC_BACSU Bacillus subtilis ydhC 26.0 63.2 204 transcriptional regulator

Detail Description Table CWU - DETL (35):

2774814 2774110 705 prf:2222216A Thermotoga maritima drrA 42.0 72.7 231 two-component system regulatory protein 2871 6371 2775689 2774937 753 sp:TIPA_STRLI Streptomyces lividans tipA 37.4 69.5 249 **transcriptional activator** 2872 6372 2776879 2775740 1140 prf:2419350A Arthrobacter sp. DK-38 30.9 53.9 382 metal-activated pyridoxal enzyme or low specificity D-Thr aldolase 2873 6373 2778504 2776768 1737 gp:ECOPOXB8G_1 Escherichia coli K12 poxB 46.3 75.8 574 pyruvate oxidase 2874 6374 2778965 2780446 1482 prf.2212334B Staphylococcus aureus plasmid 33.3 68.9 504 multidrug efflux protein pSK23 qacB 2875 6375 2780439 2780969 531 sp:YCDC_ECOLI Escherichia coli K12 ycdC 30.4 68.5 92 transcriptional regulator 2876 6376 2780996 2782315 1320 pir:D70551 Mycobacterium tuberculosis 45.6 78.4 421 hypothetical membrane protein H37Rv Rv2508c 2877 6377 2784481 2782340 2142 2878 6378 2785615 2784656 960 gp.AF096929_2 Rhodococcus erythropolis SQ1 34.3 62.1 303 3-ketosteroid dehydrogenase kstD1 2879 6379 2786355 2785651 705 sp.ALSR_BACSU Bacillus subtilis 168 alsR 37.1 69.0 232 transcriptional regulator, LysR family 2880 6380 2787782 2788594 813 pir:C70982 Mycobacterium tuberculosis 28.4 52.9 278 hypothetical protein H37Rv Rv3298c lpqC 2881 6381 2789399 2788587 813 pir:C69862 Bacillus subtilis 168 ykrA 26.7 55.6 288 hypothetical protein 2882 6382 2789935 2789477 459 2883 6383 2790152 2790550 399 pir:A45264 Oryctolagus cuniculus kidney 28.6 50.7 140 hypothetical protein cortex rBAT 2884 6384 2790946 2792448 1503 pir:B70798 Mycobacterium tuberculosis 36.0 64.0 464 hypothetical membrane protein H37Rv Rv3737 2885 6385 2792531 2792857 327 pir:S41307 Streptomyces griseus hrdB 32.3 50.3 155 transcription initiation factor sigma 2886 6386 2792873 2794327 1455 sp:TPS1_SCHPO Schizosaccharomyces pombe 38.8 66.7 487 trehalose-6-phosphate synthase tps1 2887 6387 2794300 2794812 513 2888 6388 2794870 2795637 768 sp:OTSB_ECOLI Escherichia coli K12 otsB 27.4 57.6 245 trehalose-phosphatase 2889 6389 2796749 2795676 1074 sp:CCPA_BACME Bacillus megaterium ccpA 24.7 60.2 344 glucose-resistance amylase regulator 2890 6390 2796865 2797806 942 sp:ZNUA_HAEIN Haemophilus influenzae Rd 22.4 46.7 353 high-affinity zinc uptake system HI0119 znuA protein 2891 6391 2797820 2798509 690 gp:AF121672_2 Staphylococcus aureus 8325-4 31.4 63.2 223 ABC transporter mreA 2892 6392 2798837 2799391 555 pir:E70507 Mycobacterium tuberculosis 60.0 87.4 135 hypothetical membrane protein H37Rv Rv2060 2893 6393 2799535 2801034 1500 pir:A69426 Archaeoglobus fulgidus 23.4 52.5 303 transposase (ISA0963-5) 2894 6394 2801113 2801313 201 2895 6395 2803246 2801558 1689 gp:AF096929_2 Rhodococcus erythropolis SQ1 32.1 62.0 561 3-ketosteroid dehydrogenase kstD1

2896 6396 2803996 2803250 747 2897 6397 2804691 2804074 618 pir:B72359 Thermotoga maritima MSB8 34.3 56.4 204 lipopolysaccharide biosynthesis bplA protein or oxidoreductase or dehydrogenase 2898 6398 2805110 2804676 435 sp:MI2D_BACSU Bacillus subtilis 168 idh or iolG 35.2 69.5 128 dehydrogenase or myo-inositol 2- dehydrogenase 2899 6399 2805967 2805113 855 sp:SHIA_ECOLI Escherichia coli K12 shiA 30.5 67.5 292 shikimate transport protein 2900 6400 2806441 2806016 426 sp:SHIA_ECOLI Escherichia coli K12 shiA 43.1 80.8 130 shikimate transport protein 2901 6401 2807252 2806599 654 gp:SC5A7_19 Streptomyces coelicolor A3(2) 32.6 55.7 212 transcriptional regulator SC5A7.19c 2902 6402 2808364 2807426 939 sp:PT56_YEAST Saccharomyces cerevisiae 22.8 47.3 334 ribosomal RNA ribose methylase or YOR201C PET56 tRNA/rRNA **methyltransferase** 2903 6403 2809778 2808399 1380 sp:SYC_ECOLI Escherichia coli K12 cysS 42.2 68.8 464 cysteinyl-tRNA synthetase 2904 6404 2811806 2809824 1983 prf:2511335C Lactococcus lactis sacB 47.0 77.0 668 PTS system, enzyme II sucrose protein (sucrose-specific IIABC component) 2905 6405 2813258 2811960 1299 gp:AF205034_4 Clostridium acetobutylicum 35.3 56.9 473 sucrose 6-phosphate hydrolase or ATCC 824 scrB sucrase 2906 6406 2814037 2813279 759 sp:NAGB_ECOLI Escherichia coli K12 nagB 38.3 69.4 248 glucosamine-6-phosphate isomerase 2907 6407 2815232 2814081 1152 sp:NAGA_VIBFU Vibrio furnissii SR1514 manD 30.2 60.3 368 N-acetylglucosamine-6-phosphate deacetylase 2908 6408 2815458 2816393 936 sp:DAPA_ECOLI Escherichia coli K12 dapA 28.2 62.1 298 dihydrodipicolinate synthase 2909 6409 2816409 2817317 909 sp:GLK_STRCO Streptomyces coelicolor A3(2) 28.7 57.6 321 glucokinase SC6E10.20c glk 2910 6410 2817363 2818058 696 prf:2516292A Clostridium perfringens NCTC 36.4 68.6 220 N-acetylmannosamine-6-phosphate 8798 nanE epimerase 2911 6411 2818313 2818137 177 2912 6412 2819564 2818350 1215 sp:NANH_MICVI Micromonospora viridifaciens 24.8 50.3 439 sialidase precursor ATCC 31146 nadA 2913 6413 2820285 2819557 729 gp:AF181498_1 Rhizobium etli ansR 26.6 57.2 222 L-asparagine permease operon repressor 2914 6414 2820584 2822191 1608 gp:BFU64514_1 Bacillus firmus OF4 dppA 22.5 51.4 560 dipeptide transporter protein or heme-binding protein 2915 6415 2822387 2823337 951 sp:DPPB_BACFI Bacillus firmus OF4 dappB 31.9 64.3 342 dipeptide transport system permease protein 2916 6416 2824274 2825341 1068 sp:OPPD_BACSU Bacillus subtilis 168 oppD 46.5 78.3 314 oligopeptide transport ATP-binding protein 2917 6417 2825341 2826156 816 sp:OPPF_LACLA Lactococcus lactis oppF 43.4 78.7 258 oligopeptide transport ATP-binding protein 2918 6418 2826835 2826215 621 sp:RHTB_ECOLI Escherichia coli K12 rhtB 28.5 62.7 193 homoserine/homoserin lactone efflux protein or lysE type translocator 2919 6419 2826922 2827404 483 prf:2309303A Bradyrhizobium japonicum lrp 31.0 66.2 142 leucine-responsive regulatory protein 2920 6420 2827817 2827458 360 2921 6421 2828383 2827904 480 pir:C70607 Mycobacterium tuberculosis 55.9 86.2 152 hypothetical protein H37Rv Rv3581c 2922 6422 2829146 2828379 768 sp:Y18T_MYCTU Mycobacterium tuberculosis 46.4 71.5 235 hypothetical protein H37Rv Rv3582c 2923 6423 2829749 2829156 594 pir:H70803 Mycobacterium tuberculosis 73.3 91.1 157 transcription factor H37Rv Rv3583c 2924 6424 2830057 2830779 723 prf:2214304A Mycobacterium tuberculosis 43.5 70.0 223 two-component system response H37Rv Rv3246c mtrA regulator 2925 6425 2830779 2831894 1116 sp:BAES_ECOLI Escherichia coli K12 baeS 29.3 67.7 341 two-component system sensor histidine kinase 2926 6426 2832085 2832666 582 2927 6427 2832790 2834181 1392 sp:RADA_ECOLI Escherichia coli K12 radA 41.5 74.3 463 DNA repair protein RadA 2928 6428 2834188 2835285 1098 sp:YACK_BACSU Bacillus subtilis 168 yacK 40.3 73.3 345 hypothetical protein 2929 6429 2835969 2835283 687

pir:D70804 Mycobacterium tuberculosis 29.4 53.3 231 hypothetical protein H37Rv Rv3587c 2930 6430 2837499 2836048 1452 gp:PPU96338_1 Pseudomonas putida NCIMB 59.5 85.1 471 p-hydroxybenzaldehyde 9866 plasmid pRA4000 dehydrogenase 2931 6431 2837737 2837591 147 2932 6432 2838576 2837956 621 pir:T08204 Chlamydomonas reinhardtii ca1 36.7 66.2 210 mitochondrial carbonate dehydratase beta 2933 6433 2838643 2839521 879 gp:AF121797_1 Streptomyces antibioticus IMRU 48.4 70.7 283 A/G-specific adenine glycosylase 3720 mutY 2934 6434 2839562 2840716 1155 2935 6435 2841063 2840758 306 2936 6436 2841075 2841848 774 gp:AB009078_1 Brevibacterium saccharolyticum 99.2 99.6 258 L-2.3-butanediol dehydrogenase 2937 6437 2842130 2842453 324 2938 6438 2842493 2843233 741 2939 6439 2843405 2843716 312 2940 6440 2843722 2843432 291 pir:E70552 Mycobacterium tuberculosis 48.5 69.1 97 hypothetical protein H37Rv Rv3592 2941 6441 2845139 2845558 420 GSP:Y29188 Pseudomonas aeruginosa 57.0 63.0 99 virulence factor ORF24222 2942 6442 2845889 2846101 213 GSP:Y29193 Pseudomonas aeruginosa 54.0 55.0 72 virulence factor ORF25110 2943 6443 2846186 2846506 321 GSP:Y29193 Pseudomonas aeruginosa 74.0 75.0 55 virulence factor ORF25110 2944 6444 2846940 2844166 2775 sp:MECB_BACSU Bacillus subtilis 168 mecB 58.5 86.2 832 ClpC adenosine triphosphatase/ ATP-binding proteinase 2945 6445 2847229 2848659 1431 gp:AB035643_1 Bacillus cereus ts-4 impdh 37.1 70.2 469 inosine monophosphate dehydrogenase 2946 6446 2848769 2849779 1011 pir:JC6117 Rhodococcus rhodochrous nitR 24.7 62.7 316 transcription factor 2947 6447 2850031 2851815 1785 sp:PH2M_TRICU Trichosporon cutaneum ATCC 33.5 60.9 680 phenol 2-monooxygenase 46490 2948 6448 2852017 2853732 1716 2949 6449 2853769 2855709 1941 2950 6450 2855795 2857516 1722 2951 6451 2859044 2859205 162 2952 6452 2859055 2857613 1443 gp:AF237667_1 Corynebacterium glutamicum 100.0 100.0 481 lincomycin resistance protein lmrB 2953 6453 2860145 2859195 951 pir:G70807 Mycobacterium tuberculosis 26.7 55.8 240 hypothetical protein H37Rv Rv3517 2954 6454 2862082 2860505 1578 gp:AB012100_1 Bacillus stearothermophilus lysS 41.7 71.2 511 lysyl-tRNA synthetase 2955 6455 2862929 2862132 798 gp:CGPAN_2 Corynebacterium glutamicum 29.9 52.6 268 pantoate-beta-alanine ligase

Detail Description Table CWU - DETL (39):

6688 3094050 3093175 876 pir:D70521 Mycobacterium tuberculosis 46.7 72.0 261 acyltransferase H37Rv Rv3816c 3189 6689 3095343 3094078 1266 gsp:W26465 Mycobacterium tuberculosis 70.2 87.6 419 seryl-tRNA synthetase H37Rv 3190 6690 3095574 3096287 714 sp:FARR _ECOLI Escherichia coli K12 farR 27.7 61.7 235 transcriptional regulator, GntR family or fatty acyl-responsive regulator 3191 6691 3096311 3097423 1113 pir:H70652 Mycobacterium tuberculosis 32.6 61.2 356 hypothetical protein H37Rv Rv3835 3192 6692 3097423 3097764 342 pir:A70653 Mycobacterium tuberculosis 46.0 79.7 113 hypothetical protein H37Rv Rv3836 3193 6693 3097878 3097780 99 3194 6694 3098572 3097904 669 gp:AMU73808_1 Amycolatopsis methanolica pgm 37.2 62.8 218 2,3-PDG dependent phosphoglycerate mutase 3195 6695 3098825 3099454 630 3196 6696 3099556 3100698 1143 prf:2501285A Mycobacterium smegmatis pzaA 27.4 50.9 460 nicotinamidase or pyrazinamidase 3197 6697 3100698 3101426 729 3198 6698 3101734 3102768 1035 gp:SC6G4_33 Streptomyces coelicolor A3(2) 31.6 57.1 380 transcriptional regulator SC6G4.33 3199 6699 3101863 3101744 120 3200 6700 3102630 3102079 552 3201 6701 3102894 3103763 870 3202 6702 3103926 3104252 327 pir:B26872 Streptomyces lavendulae 43.9 81.3 107 hypothetical protein ORF372 3203 6703 3104406 3105719 1314 sp:AMYH_YEAST Saccharomyces cerevisiae 28.7 55.3 432 glucan 1,4-alpha-glucosidase S288C YIR019C sta1 3204 6704

3106970 3106053 918 3205 6705 3107769 3106951 819 sp:GLPQ_BACSU Bacillus subtilis glpQ 29.0 54.1 259 glycerophosphoryl diester phosphodiesterase 3206 6706 3108131 3109519 1389 sp:GNTP_BACSU Bacillus subtilis gntP 37.3 71.9 456 gluconate permease 3207 6707 3109464 3108823 642 3208 6708 3109845 3110003 159 3209 6709 3112080 3110464 1617 sp:KPYK_CORGL Corynebacterium glutamicum 25.5 47.7 491 pyruvate kinase AS019 pyk 3210 6710 3113390 3112449 942 gsp:Y25997 Brevibacterium flavum lctA 99.7 99.7 314 L-lactate dehydrogenase 3211 6711 3113619 3115394 1776 pir:C70893 Mycobacterium tuberculosis 33.5 64.8 526 hypothetical protein H37Rv Rv1069c 3212 6712 3115407 3116042 636 gp:SC1C2_30 Streptomyces coelicolor A3(2) 32.1 58.5 224 hydrolase or haloacid SC1C2.30 dehalogenase-like hydrolase 3213 6713 3116079 3116621 543 gp:AF030288_1 Brevibacterium linens ORF1 39.9 67.6 188 efflux protein tmpA 3214 6714 3116640 3117332 693 sp:GLCC_ECOLI Escherichia coli K12 MG1655 27.6 57.0 221 **transcription activator** or glcC transcriptional regulator GntR family 3215 6715 3117336 3118121 786 pir:B70885 Mycobacterium tuberculosis 47.8 68.6 255 phosphoesterase H37Rv Rv2795c 3216 6716 3118284 3119582 1299 sp:SHIA_ECOLI Escherichia coli K12 shiA 37.9 74.4 422 shikimate transport protein 3217 6717 3119665 3120879 1215 prf:2219306A Neisseria meningitidis lldA 40.4 68.9 376 L-lactate dehydrogenase or FMN- dependent dehydrogenase 3218 6718 3120909 3121313 405 3219 6719 3121598 3121909 312 sp:RPC_BPPH1 Bacillus phage phi-105 ORF1 45.5 80.0 55 immunity repressor protein 3220 6720 3122129 3121992 138 3221 6721 3123222 3123932 711 3222 6722 3124172 3122556 1617 gp:CELY51B11A_1 Caenorhabditis elegans 29.5 51.3 569 phosphatase or reverse Y51B11A.1 transcriptase (RNA-dependent) 3223 6723 3124886 3124341 546 3224 6724 3125298 3124897 402 sp:ILL1_ARATH Arabidopsis thaliana ill 1 36.9 63.1 122 peptidase or IAA-amino acid hydrolase 3225 6725 3125343 3125492 150 3226 6726 3126145 3125495 651 sp:PMSR_ECOLI Escherichia coli B msrA 47.6 69.1 210 peptide methionine sulfoxide reductase 3227 6727 3126392 3126991 600 pir:I40858 Corynebacterium 82.3 92.7 164 superoxide dismutase (Fe/Mn) pseudodiphtheriticum sod 3228 6728 3128417 3127494 924 sp:GLTC_BACSU Bacillus subtilis gltC 32.5 65.8 292 transcriptional regulator 3229 6729 3128606 3129739 1134 gp:AF121000_10 Corynebacterium glutamicum 23.4 49.0 384 multidrug resistance transporter tetA 3230 6730 3129785 3131395 1611 3231 6731 3132920 3133030 111 3232 6732 3133028 3131508 1521 3233 6733 3133115 3133747 633 pir:G70654 Mycobacterium tuberculosis 33.8 64.8 216 hypothetical protein H37Rv Rv3850 3234 6734 3135268 3133778 1491 prf:2508244AB Streptomyces cyanogenus lanJ 27.3 59.3 447 membrane transport protein 3235 6735 3135297 3135752 456 sp:YXAD_BACSU Bacillus subtilis 168 yxaD 37.2 65.0 137 transcriptional regulator 3236 6736 3136491 3135856 636 prf:2518330B Corynebacterium diphtheriae 50.9 75.5 212 two-component system response chrA regulator 3237 6737 3136920 3137558 639 3238 6738 3137884 3138471 588 3239 6739 3137903 3136593 1311 prf:2518330A Corynebacterium diphtheriae 30.2 64.5 408 two-component system sensor chrS histidine kinase 3240 6740 3138630 3138481 150 gp.SCH69_22 Streptomyces coelicolor A3(2) 45.8 79.2 48 hypothetical protein SCH69.22c 3241 6741 3139455 3138634 822 gp:SCH69_20 Streptomyces coelicolor A3(2) 30.0 59.2 277 hypothetical protein SCH69.20c 3242 6742 3139651 3140952 1302 sp:SP3J_BACSU Bacillus subtilis spoIIIJ 26.0 53.6 265 stage III sporulation protein 3243 6743 3141523 3140885 639 pir:C70948 Mycobacterium tuberculosis 32.3 60.9 192 transcriptional repressor H37Rv Rv3173c 3244 6744 3141969 3141709 261 sp:TAG1_ECOLI Escherichia coli K12 MG1655 34.5 71.3 87 transglycosylase-associated protein tag1 3245 6745 3143356 3142454 903 sp:YW12_MYCTU Mycobacterium tuberculosis 41.2 69.6 296 hypothetical protein H37Rv Rv2005c 3246 6746 3144482 3143496 987

sp:YHBW_ECOLI Escherichia coli K12 MG1655 38.5 73.9 314 hypothetical protein yhbW 3247 6747 3144661 3145626 966 sp:YBC5_CHLVI Chlorobium vibrioforme ybc5 28.4 51.2 334 RNA pseudouridylate synthase 3248 6748 3146569 3146841 273 GSP:Y35814 Chlamydia pneumoniae 61.0 66.0 84 hypothetical protein 3249 6749 3147090 3147230 141 PIR:F81737 Chlamydia muridarum Nigg 71.0 75.0 42 hypothetical protein TC0129 3250 6750 3151575 3151369 207 3251 6751 3152204 3151842 363 sp:GLCC_ECOLI Escherichia coli K12 MG1655 30.3 56.0 109 bacterial regulatory protein, gntR glcC family or glc operon transcriptional activator 3252 6752 3152413 3153828 1416 gp:SC4G6_31 Streptomyces coelicolor 26.0 48.2 488 hypothetical protein SC4G6.31c 3253 6753 3154766 3153894 873 sp:35KD_MYCTU Mycobacterium tuberculosis 48.3 78.7 267 hypothetical protein H37Rv Rv2744c 3254 6754 3154817 3154969 153 3255 6755 3156697 3155246 1452 3256 6756 3157373 3156306 1068 3257 6757 3157471 3157223 249 3258 6758 3157787 3157479 309 3259 6759 3158124 3158834 711 gp:SCD35_11 Streptomyces coelicolor A3(2) 32.3 58.1 217 **methyltransferase** SCD35.11c 3260 6760 3159800 3159081 720 sp:NO21_SOYBN soybean NO21 26.1 55.2 241 nodulin 21-related protein 3261 6761 3160216 3160419 204 3262 6762 3160688 3161065 378 3263 6763 3160816 3161001 186 3264 6764 3160938 3160723 216 sp:TNP5_PSEAE Pseudomonas aeruginosa TNP5 48.2 92.9 56 transposon tn501 resolvase 3265 6765 3161219 3161701 483 3266 6766 3161407 3161087 321 sp:FER_SACER Saccharopolyspora erythraea fer 90.3 98.4 62 ferredoxin precursor 3267 6767 3162014 3161682 333 gp:SCD31_14 Streptomyces coelicolor A3(2) 47.3 85.5 55 hypothetical protein 3268 6768 3162694 3162804 111 GPU:AF164956_8 Corynebacterium glutamicum 81.0 84.0 27 transposase Tnp1673 3269 6769 3162710 3162871 162 GPU:AF164956_23 Corynebacterium glutamicum 84.0 90.0 46 transposase protein fragment TnpNC 3270 6770 3162852 3163889 1038 3271 6771 3162983 3162858 126 sp:G3P_PYRWO Pyrococcus woesei gap 63.2 84.2 38 glyceraldehyde-3-phosphate dehydrogenase(pseudogene) 3272 6772 3163733 3163074 660 pir:S77018 Synechocystis sp. PCC6803 32.2 59.4 180 lipoprotein sll0788 3273 6773 3166005 3163789 2217 pir:H69268 Archaeoglobus fulgidus AF0152 45.8 73.4 717 copper/potassium-transporting ATPase B or cation transporting ATPase (E1-E2 family) 3274 6774 3166437 3166267 171 3275 6775 3166978 3167169 192 3276 6776 3167646 3166450 1197 sp:BAES_ECOLI Escherichia coli K12 baeS 37.5 71.4 301 two component system sensor histidine kinase 3277 6777 3167739 3168566 828 3278 6778 3168401 3167646 756 sp:PHOP_BACSU Bacillus subtilis phoP 43.4 72.1 233 two-component response regulator or alkaline phosphatase synthesis transcriptional regulatory protein 3279 6779 3168669 3169340 672 3280 6780 3169414 3170892 1479 sp:COPA_PSESM Pseudomonas syringae pv. 26.7 47.9 630 laccase or copper resistance protein tomato copA precursor A 3281 6781 3171254 3171616 363 sp:TLPA_BRAJA Bradyrhizobium japonicum tlpA 31.7 63.4 101 thiol:disulfide interchange protein (cytochrome c biogenesis protein) 3282 6782 3172536 3171619 918 sp:QOR_MOUSE Mus musculus qor 31.4 60.9 322 quinone oxidoreductase

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PGPUB-FILING-TYPE: new

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TITLE: Methods and reagents for the rapid and efficient isolation of circulating cancer cells

PUBLICATION-DATE: November 21, 2002

INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/7.23

ABSTRACT:

Methods and compositions are provided for detecting circulating tumor cells and assessing said cells for alterations in tumor-diathesis associated molecules.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. application Ser. No. 09/248,388, filed Feb. 12, 1999, which is incorporated by reference herein. The present application also claims priority to the following U.S. Provisional Applications: 60/074,535, filed Feb. 12, 1998; 60/110,279 filed Nov. 30, 1998; 60/110,202, filed Nov. 30, 1998; 60/268,859, filed Feb. 16, 2001; 60/269,270, and 60/269,271, each filed Feb. 20, 2001. The entire disclosures of all of the foregoing provisional applications are incorporated by reference into the present specification.

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Detail Description Table CWU - DETL (13):
13TABLE XII Theraputic Targets Hormone & Hormone Regulated Proteins Androgen Receptor Cathepsin D Estrogen Receptor Estradiol Progesterone Receptor Somastatin SRC1 = **Steroid Receptor** Coactivator-1 Onco/Suppressor proteins Her-2 (cERB-b) EGFR ras c-fos c-jun c-myc p53 p63 nm23/NDP Kinase PTEN/MMAC1 SMAD4/DPC4 Notch-1 JAK3 Cell Cycle & Proliferation Cyclin A Cyclin B Cyclin C Cyclin D Cyclin E Ki67 MDR/MRP proteins Other targets PSA Prostatic Acid Phosphotase CA 125 CA 15-3 CA 27-29 HGC Cystic Fibrosis Transmembrane Regulator Laminin Receptor Neuron Specific Enolase (NSE) Alpha Fetoprotein CD99/MIC2 DHEA Prolactin CD66e/CEA Filaggrin (epidermal cells) Renal Cell Carcinoma (gp200) TAG72/CA72-4 UPA-receptor (CD87) Heregulin IPO-38 Thymidylate Synthase Topoisomerase Iia Glutathion S Transferase (GST) Lung-Resistance related Protein/Major Fault Protein (LRP/MFP) 06-Methylguanine-DNA **methyltransferase** (MGMT)

Claims Text - CLTX (67):
67. The method of claim 66, wherein said tumor diathesis associated molecule is altered and is selected from the group consisting of Androgen Receptor, Cathepsin D, Estrogen Receptor, Estradiol, Progesterone Receptor, Somastatin, **Steroid Receptor** Coactivator-I (SRCI), Her-2 (cERB-b), EGFR, ras, c-fos, c-jun, c-myc, p53, p63, nm23/NDP Kinase, PTEN/MMAC1, SMAD4/DPC4, Notch-1, JAK3, Cyclin A, Cyclin B, Cyclin C, Cyclin D, Cyclin E, Ki67, MDR/MRP proteins, PSA, Prostatic Acid Phosphatase, CA 125, CA 15-3, CA 27-29, HGC, Cystic Fibrosis Transmembrane Regulator, Laminin Receptor, Neuron Specific Enolase (NSE), Alpha Fetoprotein, CD99/MIC2, DHEA, Prolactin, CD66e/CEA, Filaggrin, gp200 TAG72/CA72-4, UPA-receptor (CD87), Heregulin, IPO-38 Thymidylate Synthase, Topoisomerase Iia, Glutathione-S-Transferase (GST), Lung-Resistance related Protein/Major Fault Protein (LRP/MFP), and 06-Methylguanine-DNA **methyltransferase** (MGMT).

Claims Text - CLTX (68):
68. The method of claim 66, wherein said tumor diathesis associated molecule is aberrantly expressed relative to wild type expression and is selected from the group consisting of Androgen Receptor, Cathepsin D, Estrogen Receptor, Estradiol, Progesterone Receptor, Somastatin, **Steroid Receptor** Coactivator-1 (SRC1), Her-2 (cERB-b), EGFR, ras, c-fos, c-jun, c-myc, p53, p63,

nm23/NDP Kinase, PTEN/MMAC1, SMAD4/DPC4, Notch-1, JAK3, Cyclin A, Cyclin B, Cyclin C, Cyclin D, Cyclin E, Ki67, MDR/MRP proteins, PSA, Prostatic Acid Phosphatase, CA 125, CA 15-3, CA 27-29, HGC, Cystic Fibrosis Transmembrane Regulator, Laminin Receptor, Neuron Specific Enolase (NSE), Alpha Fetoprotein, CD99/MIC2, DHEA, Prolactin, CD66e/CEA, Filaggrin, gp200 TAG72/CA72-4, UPA-receptor (CD87), Heregulin, IPO-38 Thymidylate Synthase, Topoisomerase Iia, Glutathione-S-Transferase (GST), Lung-Resistance related Protein/Major Fault Protein (LRP/MFP), and 06-Methylguanine-DNA **methyltransferase** (MGMT).

Claims Text - CLTX (74):

74. The method of claim 73, wherein said tumor diathesis associated molecule comprises at least two molecules selected from the group consisting of Androgen Receptor, Cathepsin D, Estrogen Receptor, Estradiol, Progesterone Receptor, Somastatin, **Steroid Receptor** Coactivator-I (SRCI), Her-2 (cERB-b), EGFR, ras, c-fos, c-jun, c-myc,p53, p63, nm23/NDP Kinase, PTEN/MMAC1, SMAD4/DPC4, Notch-1, JAK3, Cyclin A, Cyclin B, Cyclin C, Cyclin D, Cyclin E, Ki67, MDR/MRP proteins, PSA, Prostatic Acid Phosphatase, CA 125, CA 15-3, CA 27-29, HGC, Cystic Fibrosis Transmembrane Regulator, Laminin Receptor, Neuron Specific Enolase (NSE), Alpha Fetoprotein, CD99/MIC2, DHEA, Prolactin, CD66e/CEA, Filaggrin, gp200, TAG72/CA72-4, UPA-receptor (CD87), Heregulin, IPO-38, Thymidylate Synthase, Topoisomerase Iia, Glutathione-S-Transferase (GST), Lung-Resistance related Protein/Major Fault Protein (LRP/MFP), and 06-Methylguanine-DNA **methyltransferase** (MGMT).

PGPUB-DOCUMENT-NUMBER: 20020168771

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TITLE: Vectors having replication, immunogenicity and/or pathogenicity under stress promoter regulation and use thereof

PUBLICATION-DATE: November 14, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 850270

DATE FILED: May 8, 2001

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ABSTRACT:

The present invention relates to modified vectors, e.g. plasmids, viruses or microbia sucsh as yeast or bacteria, wherein the replication, immunogenicity and/or pathogenicity is placed under the control of at least one stress gene regulating element. In preferred embodiments, these modified vectors are used for gene therapy, in vaccines, or for functional genomic screening.

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Summary of Invention Paragraph - BSTX (145):

[0141] 11-beta hydroxysteroid dehydrogenase type II, 12-lipoxygenase, 17-beta hydroxysteroid dehydrogenase, 60S ribosomal protein L6,6-Omethylguanine -DNA **methyltransferase, Activating transcription factor 2, Activating transcription factor 3, Activating transcription** factor 4, Activin beta E, Activin receptor type 11, Acyl-CoA dehydrogenase, Acyl CoA Carrier Protein, Adenine nucleotide translocator 1, Alanine aminotransferase, Alcohol dehydrogenase 1, Alcohol dehydrogenase 2, Alcohol dehydrogenase 3, Alcohol dehydrogenase 4, Alcohol dehydrogenase 5, Aldehyde dehydrogenase 1, Aldehyde dehydrogenase 2, Aldehyde dehydrogenase 3, Alpha 1-antitrypsin, Alpha-1 acid glycoprotein, Alpha-1 antichymotrypsin, Alpha-catenin, Alphatubulin, Apolipoprotein A1, Apolipoprotein A11, Apolipoprotein Clil, Apolipoprotein E, Aryl hydrocarbon receptor, Aspartate aminotransferase, mitochondrial, Ataxia telangeictasia, ATP-dependent helicase 11 (70 kDa), ATP-dependent helicase 11 (Ku80), BAG-1, BAK, Bax (alpha), Bcl-2, Bcl-xL, Beta-actin, Bilirubin UDP-glucuronosyl-transferase isozyme 1, Bilirubin UDP-glucuronosyl-transferase isozyme 2, Biliverdin reductase, Branched chain acylCoA oxidase, BRCA1,

BR-cadherin, C4bbinding protein, c-abl, Calcineurin B, Calnexin, Calprotectin, Calreticulin, canalicular multispecific organic anion transporter, Carbonic Anhydrase 111, Carnitine palmitoyl-CoA transferase, Caspase 1, Caspase 2 (Nedd2), Caspase 3 (CPP32beta), Caspase 5 (ICE relIII), Caspase 6 (Mch2-alpha), Caspase 7 (Mch3alpha), Caspase 8 (FLICE), Catalase, CatecholOmethyltransferase, CCAAT/enhancer-binding protein alpha, CCAAT/enhancer-binding protein epsilon, Cell division cycle protein 2, Cell division cycle protein 20, Cell division cycle protein 25, Cellular retinoic acid binding protein 1, Cellular retinoic acid binding protein 2, cerb; c-fos, Checkpoint kinase-1, Cholesterol esterase, c-H-ras, cjun, Clusterin, c-myc, Complement component C3, Connexin 30, Connexin32, Connexin-40, Corticosteroid binding globulin, Corticotropin releasing factor, C-reactive protein, Creatine kinase b, Cyclin D1, Cyclin dependent kinase 1, Cyclin dependent kinase 4, Cyclin dependent kinase inhibitor 1A, Cyclin E, Cyclin G, Cyclin-dependent kinase 4 inhibitor (P116), Cyclindependent kinase 4 inhibitor B (P16), Cyclin-dependent kinase inhibitor P27Kip1, Cyclooxygenase 2, Cystic fibrosis transmembrane conductance regulator, Cytochrome P450 11A1, Cytochrome P450 17A, Cytochrome P450 1A1, Cytochrome P450 1A2, Cytochrome P450 1 B1, Cytochrome P450 2A1, Cytochrome P450 2A3, Cytochrome P450 2A6, Cytochrome P450 2131, Cytochrome P450 21310, Cytochrome P450 2132, Cytochrome P450 2C11, Cytochrome P450 2C12, Cytochrome P450 2C19, Cytochrome P450 2C9, Cytochrome P450 2D6, Cytochrome P450 2E1, Cytochrome P450 2F2, Cytochrome P450 3A1, Cytochrome P450 3A4, Cytochrome P450 4A, Cytochrome P450 4A1, Damage specific DNA binding protein p48 subunit, Defender against cell death-1, Deleted in colorectal cancer, Deltalike protein, Dihydrofolate reductase, Disulfide isomerase related protein (ERp72), DNA binding protein inhibitor ID2, DNA dependent helicase, DNA dependent protein kinase, DNA ligase 1, DNA ligase IV, DNA mismatch repair protein (MLH1), DNA mismatch repair protein (PMS2), DNA mismatch repair/binding protein (MSH3), DNA polymerase alpha, DNA polymerase beta, DNA polymerase beta, DNA repair and recombination homologue (RAD 52), DNA repair helicase II ERCC-3, DNA repair protein (RAD 50), DNA repair protein (XRCC1), DNA repair protein XP-D, DNA replication factor C (36 kDa), DNA topoisomerase 1, DNA topoisomerase 11, Dopamine beta-hydroxylase, DRA, Dynein light chain 1, E2F, Early growth regulated protein 1, E-Cadherin, ECE-1 (endothelin converting enzyme), Endothelin-1, Enolase alpha, Enoyl CoA hydratase, Eotaxin, Epidermal growth factor, Epoxide hydrolase, ERA-B, ERCC 1 (excision repair protein), ERCC 3 (DNA repair helicase 11), ERCC 5 (excision repair protein), ERCC 6 (excision repair protein), ERK1, Erythropoietin, Erythropoietin receptor, ESelectin, Estrogen receptor, Farnesol receptor, Fas antigen, Fas associated death domain (FADD), Fas ligand, Fas/Apo1 receptor, Fatty acid synthase, Fatty acyl-CoA oxidase, Fatty acyl-CoA synthase, FEN-1 (endonuclease), Fibrinogen gamma chain, Fibronectin receptor, FIC1, Filagrin, Flavin containing monooxygenase 1, Flavin containing monooxygenase 3, FosB, Fra-1, Fucosyl transferase (alpha-1,2fucosyltransferase), Gadd153, Gadd45, Gamma-glutamyl hydrolase precursor, Gamma-glutamyl transpeptidase, GCLR, GCLS, **Glucocorticoid receptor,** Glucose-6-phosphate dehydrogenase, Glucose-regulated protein 170, Glucose-regulated protein 58, Glucose-regulated protein 78, Glucoseregulated protein 94, Glutamicoxaloacetic transaminase, Glutaminc-pyruvic transaminase, Glutathione peroxidase, Glutathione reductase, Glutathione S-transferase alpha subunit, Glutathione S-transferase 4a, Glutathione synthetase, Glyceraldehyde 3-phosphate dehydrogenase, GOS24 (zinc finger transcriptional regulator), Granulocyte-macrophage colony-stimulating factor, Growth-arrested-specifi- c protein 1, Growth-arrested-specific protein 3, GT mismatch binding protein, H-cadherin, Heat shock protein 12, Heat shock

protein 47, Heat shock protein 70, Heat shock protein 70.1, Heat shock protein 90, Helicase-like transcription factor, Heme binding protein 23, Heme oxygenase-1, Hepatic lipase, Hepatocyte growth factor, Hepatocyte growth factor activator, Hepatocyte growth factor receptor, Hepatocyte nuclear factor 4, Histone 2A, Histone 28, HMG CoA reductase, Hydroxyacyl CoA dehydrogenase, Hydroxysteroid sulfotransferase a, Hypoxanthine-guanine phosphoribosyltransferase, ICE-rel 11 (Caspase 4), ICH-2 cysteine protease=CASPASE 4, IkB-a, Insulin-like growth factor binding protein 1, Insulin-like growth factor binding protein 2, Insulin-like growth factor binding protien 3, Insulin-like growth factor I, Insulin-like growth factor 11, Integrin alpha, Integrin alpha L, Integrin betas, Integrin beta2, Intercellular adhesion molecule-1, Intercellular adhesion molecule-2, Intercellular adhesion molecule-3, Interferon gamma, Interferon inducible protein 10, Interferon inducible protein 15, Interleukin-1 alpha, Interleukin-12, Interleukin-2, Interleukin-4, Interleukin-5, Interleukin-6, Involucrin, JNK1 stress activated protein kinase, K-cadherin, Ki67, Lactate Dehydrogenase 8, Lactoferrin, Lipopolysaccharide binding protein, Lipoprotein lipase precursor, Liver fatty acid binding protein, L-myc, Low density lipoprotein receptor, Luteinizing hormone, Lysyl oxidase, Macrophage inflammatory protein-1 alpha, Macrophage inflammatory protein-1 beta, Macrophage inflammatory protein-2 alpha, Macrophage inflammatory protein-2 beta, Macrophage inflammatory protein-3 alpha, Macrophage inflammatory protein-3 beta, Malic enzyme, MAP kinase kinase, Matrix metal loproteinase1, Matrix metal loproteinase-2, MDM-2, MET proto-oncogene, Metallothionein 1, Metallothionein 2, Metallothionein 3, Metallothionein IA, Metallothionein IG, Metalregulatory **transcription factor-1, Mitogen activated** protein kinase (P38), Mitogen inducible gene (mig-2), MOAT-B (MRP/organic anion transporter), Monoamine oxidase A, Monoamine oxidase B, Multidrug resistance-associated protein, Multidrug resistant protein-1, Multidrug resistant protein-2, Multidrug resistant protein-3 =cMOAT2, MUTL homologue (MLH1), MutS Homologue (MSH2), Myeloid cell differentiation protein-1, Na/taurocholate cotransporting polypeptide, NADPH cytochrome P450 -oxidoreductase, NADPH cytochrome P450 reductase, NADPH quinone oxidoreductase-1 (DTDiaphorase), Natural killer cell-enhancing factor B, N-cadherin, NF-kappaB (p65), Nitric oxide synthase-1, inducible, Nucleoside diphosphate kinase beta isoform, 0-6-alkylguanine-DNAalkyltran- sferase, OBcadherin 1, OB-cadherin 2, Octamer binding protein 1, Octamer binding protein 2, Octamer binding protein 3, Oncostatin M, Organic anion transporter 1, Organic anion transporter 3, Organic anion transporter K1, Organic anion transporting polypeptide 1, Organic cation transporter 1, Organic cation transporter 2, Organic cation transporter 3, Organic cation transporter N1, Organic cation transporter N2, Ornithine decarboxylase, Osteopontin, Oxygen regulated protein 150, p53, PAPS synthetase, P-cadherin, PEGS (progression elevated gene 3), Peroxisomal 3-ketoacyl-CoA thiolase 1, Peroxisomal 3-ketoacylCoA thiolase 2, Peroxisomal acyl-CoA oxidase, Peroxisomal fatty acyl-CoA oxidase, Peroxisome assembly factor 1, Peroxisome assembly factor 2, Peroxisome biogenesis disorder protein-1, Peroxisome biogenesis disorder protein-11, Peroxisome biogenesis disorder protein-4, Peroxisome hydratase, Peroxisome proliferator activated receptor alpha, Peroxisome proliferator activated receptor gamma, Phenol sulfotransferase, Phosphoenolpyruvate carboxykinase, Phosphoglyceride kinase, Phospholipase A2, Plasminogen activator inhibitor 2, Platelet derived growth factor B, Platelet/endothelial cell adhesion molecule-1, Poly (ADP ribose) polymerase, Proliferating cell nuclear antigen gene, Prostaglandin H synthase, Protein kinase C betal,

Protein-tyrosine phosphatase, Putative protein tyrosine phosphatase, RAID, RAID 51 homologue, RANTES, Ref 1, Replication factor C, 40-kDa subunit (AI), Replication protein A (70 kDa subunit), Retinoblastoma, Retinoblastoma related protein (P 107), Retinoid X receptor alpha, Retinoid X receptor beta, Retinoid X receptor gamma, Ribonucleotide reductase M1 subunit, Ribosomal protein L13A, Ribosomal protein S9, RNA-dependent helicase, ROAT1 (renal organic anion transporter), Serum amyloid A1, Serum amyloid A2alpha, Sister of p-glycoprotein, Sodium/bile acid cotransporter, Sonic hedgehog gene, SQM1, Superoxide Dismutase Cu/Zn, Superoxide dismutase Mn, T-cell cyclophilin, Tenascin, Thiopurine **methyltransferase,** Thioredoxin, Thrombospondin 2, Thymidine kinase, Thymidylate synthase, Thymosin beta-10, Tissue inhibitor of metalloproteinases-1, Tissue transglutaminase, Transcription factor IID, Transferrin, Transforming growth factor-beta 3, Tumor necrosis factor associated factor 2 (TRAF2), Tumor necrosis factor receptor 1, Tumor necrosis factor receptor 2, Tumor necrosis factor receptor-1 associated protein (TRADD), Tumor necrosis factor-alpha, Tumor necrosis factorbeta, Type 1 interstitial collagenase, Tyrosine aminotransferase, Tyrosine protein kinase receptor (UFO), Ubiquitin, Ubiquitin conjugating enzyme (Rad 6 homologue), Ubiquitin-homology domain protein PIC1, UDPglucuronosyltransferase 1, UDP-glucuronosyltransferase 1A6, UDPglucuronosyltransferase 2, UDP-glucuronosyltransferase 28, Uncoupling protein 1, Uncoupling protein 2, Uncoupling protein 3, Urate oxidase, UV excision repair protein RAD 23 (XP-C), Vascular cell adhesion molecule 1 (VCAM-1), Vascular endothelial growth factor, Vascular endothelial growth factor D, Very long-chain acyl-CoA dehydrogenase, Vimentin, Vitellogenin, Waf1, XRCC1 (DNA repair protein).

PGPUB-DOCUMENT-NUMBER: 20020165355

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020165355 A1

TITLE: Methylated, SmD homologous peptides, reactive with the antibodies from sera of living beings affected with systemic lupus erythematosus

PUBLICATION-DATE: November 7, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Meheus, Lydie	Merelbeke		BE	
Luhrmann, Reinhard Georg	Marburg		DE	
Union, Ann	Aalter		BE	
Raymackers, Joseph	Eke		BE	

APPL-NO: 10/ 056407

DATE FILED: January 24, 2002

RELATED-US-APPL-DATA:

child 10056407 A1 20020124

parent division-of 09297981 19990510 US GRANTED

parent-patent 6362007 US

child 09297981 19990510 US

parent a-371-of-international PCT/EP98/05518 19980831 WO UNKNOWN

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
EP	97870127.4	1997EP-97870127.4	August 29, 1997

US-CL-CURRENT: 530/350

ABSTRACT:

The present invention relates to a method of producing certain peptides containing methylated arginines that are followed by a glycine residue and that constitute immunogenic determinants of antibodies present in sera from patients with systemic lupus erythematosus, or Epstein-Barr virus and wherein the methylation is a prerequisite for reacting with said antibodies. The invention also relates to the use of said peptides for diagnosis and treatment of systemic lupus erythematosus and related diseases, and diseases in which Epstein-Barr virus has been implicated.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (19):

[0018] According to a more specific embodiment the present invention also relates to a method for producing any of the above mentioned peptides, by classical chemical synthesis, wherein methylated arginines are substituted for unmethylated arginine residues at certain steps during the chemical synthesis. The present invention also relates to a method for producing any of the above mentioned peptides, wherein the primary amino acid sequence is produced by classical chemical synthesis, and wherein the arginine residues that precede glycine residues are subsequently methylated by contacting said peptides with a protein **arginine methyltransferase**. The present invention also relates to a method for producing any of the above mentioned peptides comprising the following steps: (i) transforming an appropriate cellular host with a recombinant vector in which a polynucleic acid is inserted comprising the sequence that codes for said peptide under the control of the appropriate regulatory elements such that said peptide or a protein comprising said peptide is expressed and/or secreted, (ii) culturing said transformed cellular host under conditions allowing expression of said protein or peptide and allowing a partial or optimal methylation of the arginines present in said peptide, and (iii) harvesting said peptide. The present invention also relates to a method for producing any of the above mentioned peptides comprising the following steps: (i) transforming an appropriate cellular host with a recombinant vector in which a polynucleic acid is inserted comprising the sequence that codes for said peptide under the control of the appropriate regulatory elements, such that said peptide or a protein comprising said peptide is expressed and/or secreted, (ii) culturing said transformed cellular host under conditions allowing expression of said protein or said peptide, (iii) harvesting said protein or said peptide, and (iv) methylating arginine residues of said protein or said peptide by contacting with a protein **arginine methyltransferase**. According to a more specific embodiment the present invention also relates to any of the above mentioned methods, wherein said host cell is a bacterial host or yeast or any other eukaryotic host cell which is preferably transformed with a recombinant baculovirus.

Claims Text - CLTX (9):

8) Method for producing a peptide according to any of claims 1 to 6, wherein the primary amino acid sequence is produced by classical chemical synthesis, and wherein the arginine residues that precede glycine residues are subsequently methylated by contacting said peptide with a protein **arginine methyltransferase**.

Claims Text - CLTX (11):

10) Method for producing a peptide of any of claims 1 to 6 comprising the following steps: transforming an appropriate cellular host with a recombinant vector in which a polynucleic acid is inserted comprising the sequence that codes for said peptide under the control of the appropriate regulatory elements, such that said peptide or a protein comprising said peptide is

expressed and/or secreted, culturing said transformed cellular host under conditions allowing expression of said protein or said peptide, harvesting said protein or said peptide, methylating arginine residues of said protein or said peptide by contacting with a protein **arginine methyltransferase**.

PGPUB-DOCUMENT-NUMBER: 20020164575

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020164575 A1

TITLE: Gene identification

PUBLICATION-DATE: November 7, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Case, Casey C.	San Mateo	CA	US	
Urnov, Fyodor	Richmond	CA	US	

APPL-NO: 09/ 942090

DATE FILED: August 28, 2001

RELATED-US-APPL-DATA:

child 09942090 A1 20010828

parent continuation-in-part-of 09395448 19990914 US PENDING

US-CL-CURRENT: 435/4, 435/6

ABSTRACT:

The present disclosure provides methods and compositions for identifying a particular genomic sequence as a gene and/or a coding region, once that sequence has been tentatively identified as a gene based on genomic analysis using one or more gene prediction algorithms. The methods include the use of exogenous molecules such as zinc finger proteins which are capable of binding to and modulating expression of gene transcription, targeted to putative gene sequences, followed by assay for one or more selected phenotypes.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. patent application Ser. No. 09/395,448, filed Sep. 14, 1999, the disclosure of which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (50):
[0081] A "**transcripti nal activator" and a "transcriptional** repressor" refer to proteins or functional fragments of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g.,

transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (114):

[0145] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20020160940

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020160940 A1

TITLE: Modulation of endogenous gene expression in cells

PUBLICATION-DATE: October 31, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Case, Casey C.	San Mateo	CA	US	
Wolffe, Alan	Richmond	CA	US	
Urnov, Fyodor	Richmond	CA	US	
Lai, Albert	Richmond	CA	US	
Snowden, Andrew	Alameda	CA	US	
Tan, Siyuan	El Cerrito	CA	US	
Gregory, Philip			US	

APPL-NO: 09/ 942087

DATE FILED: August 28, 2001

RELATED-US-APPL-DATA:

child 09942087 A1 20010828

parent continuation-in-part-of 09229037 19990112 US PENDING

US-CL-CURRENT: 514/6, 435/455

ABSTRACT:

Disclosed herein are methods and compositions for modulating expression of endogenous cellular genes using recombinant zinc finger proteins.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. patent application Ser. No. 09/229,037, filed Jan. 12, 1999, the disclosure of which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (53):

[0097] A "**transcriptional activator" and a "transcripti nal** repressor" refer to proteins or functional fragments of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g.,

transcription factors and co-factors (e.g., KRAB, MAD, ERD, SfD, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP 64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (107):

[0151] Common regulatory domains for addition to the ZFP include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20020160378

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020160378 A1

TITLE: Stress-regulated genes of plants, transgenic plants containing same, and methods of use

PUBLICATION-DATE: October 31, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Harper, Jeffrey F.	Del Mar	CA	US	
Kreps, Joel	Carlsbad	CA	US	
Wang, Xun	San Diego	CA	US	
Zhu, Tong	San Diego	CA	US	

APPL-NO: 09/ 938842

DATE FILED: August 24, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60227866 20000824 US

non-provisional-of-provisional 60264647 20010126 US

non-provisional-of-provisional 60300111 20010622 US

US-CL-CURRENT: 435/6

ABSTRACT:

Clusters of plant genes that are regulated in response to one or more stress conditions are provided, as are isolated plant stress-regulated genes, including portions thereof comprising a coding sequence or a regulatory element, and to consensus sequences comprising a plant stress-regulated regulatory element. In addition, a recombinant polynucleotide, which includes a plant stress-regulated gene, or functional portion thereof, operatively linked to a heterologous nucleotide sequence, is provided, as are transgenic plants, which contain a plant stress-regulated gene or functional portion thereof that was introduced into a progenitor cell of the plant. Also provided are methods of using a plant stress-regulated gene to confer upon a plant a selective advantage to a stress condition, methods of identifying an agent that modulates the activity of a plant stress-regulated regulatory element, and methods of determining whether a plant has been exposed to a stress.

[0001] This application claims the benefit under 35 U.S.C. 119(e) of U.S. Ser. No. 60/227,866, filed Aug. 24, 2000; U.S. Ser. No. 60/264,647, filed Jan. 26, 2001; and U.S. Ser. No. 60/300,111, filed Jun. 22, 2001, each of

which is incorporated herein by reference in its entirety.

---------- KWIC ---------

Detail Description Table CWU - DETL (7):
796 putative trypsin inhibitor 797 unknown protein 798 putative multispanning membrane protein 799 receptor-like kinase, putative 800 putative inosine-5-monophosphate dehydrogenase 801 inosine-5'-monophosphate dehydrogenase, putative 802 amino acid permease 6 (emb.vertline.CAA65051.1) 803 NADPH-ferrihemoprotein reductase (ATR2) 804 putative WRKY-type DNA binding protein 805 putative ankyrin 806 putative hexose transporter 807 aquaporin/MIP - like protein 808 Ser/Thr protein kinase isolog 809 pectate lyase like protein 810 putative 60S ribosomal protein L17 811 putative protein 812 unknown protein 813 phenylalanine ammonia-lyase 814 putative cytochrome P450 monooxygenase 815 ARR1 protein, putative 816 putative bHLH transcription factor 817 aminomethyltransferase-like precursor protein 818 purple acid phosphatase precursor 819 AP2 domain containing protein, putative 820 ubiquitin-conjugating enzyme E2-21 kD 1 (ubiquitin-protein ligase 4) (ubiquitin carrier protein 4) (sp.vertline.P42748) 821 translation initiation factor 822 putative VAMP-associated protein 823 spermidine synthase, putative 824 putative protein 825 unknown protein 826 AtKAP alpha 827 glyceraldehyde-3- phosphate dehydrogenase, putative 828 putative poly(A) binding protein 829 aipha-tubulin, putative 830 serine/threonine-specific protein kinase ATPK64 (pir.vertline..vertline.S20918) 831 putative aspartate-tRNA ligase 832 ras-related small GTP- binding protein RAB1c 833 cycloartenol synthase 834 No function assigned by TIGR 835 cytochrome P450 836 GTPase AtRAB8 837 3-phosphoserine phosphatase 838 transcription factor CRC 839 nuclear cap-binding protein; CBP20 (gb.vertline.AAD29697.1) 840 chioroplast membrane protein (ALBINO3) 841 biotin holocarboxylase synthetase 842 expansin AtEx6 843 unknown protein 844 mercaptopyruvate sulfurtransferase, putative 845 putative thiosulfate sulfurtransferase 846 dihydrolipoamide 5- acetyltransferase 847 auxin transport protein REH1, putative 848 putative auxin transport protein 849 apyrase (Atapy1) 850 root cap 1 (RCP1) 851 hypothetical protein 852 putative protein 853 predicted protein of unknown function 854 hypothetical protein 855 hypothetical protein 856 hypothetical protein 857 putative aldehyde dehydrogenase 858 putative peroxidase 859 UDP-glucose 4-epimerase - like protein 860 indole-3-acetate beta- glucosyltransferase like protein 861 putative beta-1,3-glucanase 862 disease resistance protein-like 863 putative respiratory burst oxidase protein B 864 ubiquitin-conjugating enzyme UBC3 865 cytoplasmic aconitate hydratase 866 NADPH oxidoreductase, putative 867 PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT -like 868 putative protein 869 unknown protein 870 60S acidic ribosomal protein P2 871 No function assigned by TIGR 872 1,4-alpha-glucan branching enzyme protein soform SBE2.2 precursor 873 calcium binding protein (CaBP-22) 874 putative phosphoglucomutase 875 shaggy-like protein kinase etha (EC 2.7.1.-) 876 pyruvate decarboxylase (gb.vertline.AAB16855.1) 877 hypothetical protein 878 putative protein kinase 879 putative protein kinase 880 putative leucine aminopeptidase 881 probable cytochrome P450 882 protein kinase 6-like protein 883 **arginine methyltransferase** (pam 1) 884 MYB96 transcription factor-like protein 885 putative protein 886 metal ion transporter 887 No

function assigned by TIGR 888 flax rust resistance protein, putative 889 fructose-2,6- homolog bisphosphatase, putative 890 exonuclease RRP41 891 squamosa promoter binding protein-like 2 (emb.vertline.CAB56576.1) 892 putative squamosa- promoter binding protein 893 O-acetylserine(thiol) lyase, putative 894 snoRNA 895 snoRNA 896 ferredoxin-NADP + reductase 897 H+-transporting ATP synthase chain 9 - like protein 898 photosystem I subunit III precursor, putative 899 photosystem I subunit VI precursor 900 auxin-binding protein 1 precursor 901 putative RAS superfamily GTP- binding protein 902 disease resistance protein-like 903 protein kinase like protein 904 glucuronosyl transferase-like protein 905 putative homeodomain transcription factor 906 putative flavonol reductase 907 putative protein 908 salt-tolerance protein 909 40S ribosomal protein S30 910 putative bZIP transcription factor 911 putative protein 912 putative cinnamoyl CoA reductase 913 unknown protein 914 putative RNA-binding protein 915 phosphatidylinositol synthase (PIS1) 916 unknown protein 917 hydroxyproline-rich glycoprotein 918 50S ribosomal protein L15, chloroplast precursor 919 unknown protein 920 putative YME1 ATP-dependant protease 921 unknown protein 922 putative ribosomal protein L28 923 unknown protein 924 putative protein 925 protein ch-42 precursor, chloroplast 926 protein serine/threonine kinase, putative 927 beta-VPE 928 putative vacuolar sorting receptor 929 putative translation initiation factor IF-2 930 predicted protein of unknown function 931 putative protein 932 hypothetical protein 933 hypothetical protein 934 phosphate transporter, putative

PGPUB-DOCUMENT-NUMBER: 20020155119

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020155119 A1

TITLE: Isolation and use of fetal urogenital sinus expressed sequences

PUBLICATION-DATE: October 24, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Sikes, Robert A.	Gordonsville	VA	US	
Chung, Leland W.K.	Lovingston	VA	US	
Kim, Jin Hee	Santa Monica	CA	US	
Fasciana, Claudia	Rotterdam		NL	
Trapman, Jan	Mijnsheerenland		NL	

APPL-NO: 09/ 933797

DATE FILED: August 22, 2001

RELATED-US-APPL-DATA:

child 09933797 A1 20010822

parent continuation-of 09482933 20000114 US ABANDONED

child 09482933 20000114 US

parent continuation-of PCT/US99/10746 19990514 US UNKNOWN

non-provisional-of-provisional 60085383 19980514 US

US-CL-CURRENT: 424/185.1, 435/320.1 , 435/325 , 435/6 , 435/69.1 , 530/350 , 536/23.5

ABSTRACT:

The invention comprises methods for identifying biomarkers useful for prognostic or diagnostic assays of human prostate disease, and for identifying those fetal genes which are differentially expressed between prostate cancers versus normal or benign prostate.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit under 35 U.S.C. section 119(e) of co-pending U.S. provisional application Ser. No. 60/085,383, filed May 14, 1998, the entire text of which is herein incorporated by reference without disclaimer.

---------- KWIC ---------

Detail Description Table CWU - DETL (2):
locus protein 3) (265 aa) 1.4e-13 ugs188 RS18_HUMAN P25232 homo sapiens (human), rattus norvegicus (rat), and mus musculus 40S ribosomal protein S18 (KE3) (152 aa) 1.3e-21 ugs226 RS24_XENLA P02377 xenopus laevis (african clawed frog). 40s ribosomal protein S24 (S19) (132 aa) 4e-27 Transcription Factors ua1a2 SON_HUMANP 18583 homo sapiens (human) son protein (son3). DNA binding protein w/mos and myc homology 11/1995 (1523 aa) 2.3e-13 ug027rcon PUR_MOUSE P42669 mus musculus (mouse). **transcriptional activator** protein (321 aa) 3.1e-07 ug087rcon TYY1_MOUSE Q00899 mus musculus (mouse). transcriptional repressor protein (414 aa) 2.5e-33 ug113rcn1o POL2_MOUSE P11369 mus musculus (mouse). retrovirus-related pol polyprotei (1300 aa) 8.8e-36 ug228 ZN83_HUMAN P51522 homo sapiens (human). zinc finger protein 83 (zinc fing (428 aa) 6.4e-08 ug243 POL2_MOUSE P11369 mus musculus (mouse). retrovirus-related pol polyprotei (1300 aa) 7.1e-51 ug249 POL2_MOUSE P11369 mus musculus (mouse). retrovirus-related pol polyprotei (1300 aa) 1.8e-10 ug271 CABA_MOUSE Q99020 mus musculus (mouse). carg-binding factor-a (cbf-a). 11 (285 aa) 3.5e-08 *ug277t HXAD_AMBME P50210 ambystoma mexicanum (axolotl). homeotic protein hox-a13 (107 aa) 1.2e-34 (other locus 1399859 Acc #U59322) ug289 SN21_HUMAN P28370 homo sapiens (human). possible global transcription activator (976 aa) 1.9e-09 ug313 POL2_MOUSE P11369 mus musculus (mouse). retrovirus-related pol polyprotei (1300 aa) 2.7e-37 ug367 ETF_MOUSE P48301 mus musculus (mouse). embryonic tea domain- containing factor (445 aa) 2.1e-23 ug486 CL36_RAT P52944 rattus norvegicus (rat). lim protein clp36. (contains homeodomain of lin-11) 10/1996 (327 aa) 2e-24 ugs101 POL2_MOUSE P11369 mus musculus (mouse). retrovirus-related pol polyprotei (1300 aa) 5.8e-23 Mitochondrial ug002rcon ATP6_MOUSE P00848 mus musculus (mouse). atp synthase a chain (ec 3.6.1.34 (226 aa) 1.2e-52 ug007rcon CYB_MOUSE P00158 mus musculus (mouse). cytochrome b (ec 1.10.2.2). 3/1992 (381 aa) .8e-85 ug045con NU5M_MOUSE P03921 mus musculus (mouse). nadh-ubiquinone oxidoreductase ch (607 aa) 5.1e-37 ug063rcon GR75_MOUSE P38647 mus musculus (mouse). mitochondrial stress-70 protein p (679 aa) 3.4e-31 ug103rcon ATP6_MOUSE P00848 mus musculus (mouse). atp synthase a chain (ec 3.6.1.34 (226 aa) 1.1e-19 ug207 NU5M_MOUSE P03921 mus musculus (mouse). nadh-ubiquinone oxidoreductase ch (607 aa) 8.9e-55 ug296 ATP6_MOUSE P00848 mus musculus (mouse). atp synthase a chain (ec 3.6.1.34 (226 aa) 7e-27 ug336 ATP6_MOUSE P00848 mus musculus (mouse). atp synthase a chain (ec 3.6.1.34 (226 aa) 7.2e-32 ug363 NU4M_MOUSE P03911 mus musculus (mouse). nadh-ubiquinone oxidoreductase ch (459 aa) 1.4e-46 ug378 ATPQ_RAT P31399 rattus norvegicus (rat). atp synthase d chain, mitochondr (160 aa) 2.8e-11 ug489 NU1M_MOUSE P03888 mus musculus (mouse). nadh-ubiquinone oxidoreductase ch (315 aa) 4.5e-61 ug510 COX3_MOUSE P00416 mus musculus (mouse). cytochrome c oxidase polypeptide (261 aa) 2.8e-11 ugs064 ATP6_MOUSE P00848 mus musculus (mouse). atp synthase a chain (ec 3.6.1.34 (226 aa) 1.1e-18 ugs091 NU6M_MOUSE P03925 mus musculus (mouse). nadh-ubiquinone oxidoreductase ch (172 aa) 3.7e-32 ugs094 ATP6_MOUSE P00848 mus musculus (mouse). atp synthase a chain (ec 3.6.1.34 (226 aa) 4.6e-19 RNA Splicing, Binding, RNPs, etc... ug072rcon P68_HUMAN P17844 homo sapiens (human). p68 protein (rna helicase). 6/1994 (614 aa) 1.2e-16 ug145 HMT1_YEAST P38074 saccharomyces cerevisiae

(baker's yeast). hnrnp arginine n-**methyltransferase** (348 aa) 4.2e-17 ug225 ROA1_MOUSE P49312 mus musculus (mouse). heterogeneous nuclear ribonucleop (319 aa) 3.7e-15 ug293 PSF_HUMAN P23246 homo sapiens (human). ptb-associated splicing factor (ps (707 aa) 1.3e-41 ug310 FUS_HUMAN P35637 homo sapiens (human). ma-binding protein fus/tls. 11/19 (526 aa) 1.7e-27 *ug311icons PSF_HUMAN P23246 homo sapiens (human). ptb-associated splicing factor (ps (707 aa) 1.7e-25 ug391 RSMB_MOUSE P27048 mus musculus (mouse). small nuclear ribonucleoprotein a (231 aa) 2.6e-25 *ug485ors RNPL_HUMAN P98179 homo sapiens (human). putative rna-binding protein rnpl (157aa) 3.1e-12 ugs115 UBIQ_HUMAN P02248 homo sapiens (human), bos taurus (bovine), UBIQUITIN (76 aa) 3e-14 ugs128 P68_HUMAN P17844 homo sapiens (human). p68 protein (rna helicase). 6/1994 (614 aa) 2.6e-13 Peptidases, Proteinases, Isomerases, Transferases *ug101rcon DPP4_MOUSE P28843 mus musculus (mouse). dipeptidyl peptidase iv (ec 3.4.1) (760 aa) 5.7e-07 ug153rcon PPI1_MOUSE P53810 mus musculus (mouse). phosphatidylinositol (ptdins) transfer protein alpha (270 aa) 9.2e-26 ug188rcon NMT_HUMAN P30419 homo sapiens (human). glycylpeptide n-tetradecanoyltransferase (peptide N- myristoyltransferase) (NMT) (416 aa) 1e-51 ug211 COGT_MOUSE P53690 mus musculus (mouse). matrix metalloproteinase-14 precu (582 aa) 3.2e-51 *ug335 NEP_RAT P07861 rattus norvegicus (rat). neprilysin (ec 3.4.24.11) (neutral endopeptidase) (749 aa) 5e-20 ug458 VKGC_HUMAN P38435 homo sapiens (human). vitamin k-dependent gamma glutamyl-carboxylase (758 aa) 1.7e-34 ugs030 PUR6_RAT P51583 r multifunctional protein ade2 (amidophosphoribosyltransferase) Cell cycle dependent regulation (425 aa) 1.7e-16 ugs123 PDI_MOUSE P09103 m protein disulfide isomerase precursor (pdi). (509 aa) 5e-11 ugs180 AMP2_RAT P38062 rattus norvegicus (rat). methionine aminopeptidase 2 (478 aa) 7.2e-27 ugs190 FUCO_HUMAN P04066 homo sapiens (human). tissue alpha-1-fucosidase precurs (Lysosomal storage) (461 aa) 6.8e-25 Chromosomal Associated ug040rcon RCC_MESAU P23800 mesocricetus auratus (golden hamster). regulator of chromosomal condensation (421 aa) 4.8e-07 ugs010 H33_HUMAN P06351 homo sapiens (human), mus musculus (mouse), rattus norve histone H3.3 (H3b) (135 aa) 4.3e-18 ugs146 TPR_HUMAN P12270 homo sapiens (human). nucleoprotein tpr. 10/1996 (2349 aa) 1.9e-15 Heat Shock, Chaperones, Stress-Induced ugo42con HS9B_MOUSE P11499 mus musculus (mouse). heat shock protein hsp 84 (tumor specific transplantation antigen) (723 aa) 3.7e- 51 ug356 HS7C_RAT P08109 rattus norvegicus (rat), and mus musculus (mouse). heat shock cognate 71kDa (646 aa) 6.3e-58 Neural Specific ug379 HIPP_HUMAN P41211 homo sapiens (human). neuron specific calcium- binding protein hippocalcin (BDR-2) (192 aa) 9.2e-09 ugs023 NED4_MOUSE P46935 mus musculus (mouse). nedd-4 protein (ec6.3.2.-) neural precursor cell protein (frag (957 aa) 4.8e-19 Hypothetical *ug093rcon YO11_MOUSE P11260 mus musculus (mouse). hypothetical protein orf-1137. (L1Md domain protein, repetitive element retroposon- like) 7/ (379 aa) 4.4e-46 ug095rcon YJZ4_YEAST P47095 saccharomyces cerevisiae (baker's yeast). hypothetical (244 aa) 8.3e-18 ug309 YNK7_YEAST P53930 saccharomyces cerevisiae (baker's yeast). hypothetical (226 aa) 2.5e-14 ug412 YCFB_HAEIN P44551 haemophilus influenzae. hypothetical protein hi0 174. 10 (418 aa) 6.5e-11 Nucleotide metabolism (Cytosolic) ug084rcon THIO_MOUSE P10639 inns musculus (mouse). thioredoxin (atl-derived factor) ribont-deoxyribont converter and general reducer (104 aa) 2.3e-21 ug413 ARF5_HUMAN P26437 homo sapiens (human), and rattus norvegicus (rat). adp-ribosylation factor 5 (179 aa) 5.2e-07 Unknown ug480 IGEB_MOUSE P03975 mus musculus (mouse). IgE-binding protein. 4/1988 (557 aa) 1.5e-24 ugs044 TLM_MOUSE P17408 mus musculus (mouse). tlm protein (tlm oncogene). 12/199

(317aa)1.4e-07 Vector Associated (Tet-R/Beta-gal) ug016_38_80 TER1_ECOLI
P03038 escherichia coli , tetracycline repressor

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TITLE: Methods of using randomized libraries of zinc finger proteins for the identification of gene function

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INVENTOR-INFORMATION:

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DATE FILED: December 6, 2000

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US-CL-CURRENT: 435/6, 435/4 , 435/455

ABSTRACT:

The present invention relates to methods of using libraries of randomized zinc finger proteins to identify genes associated with selected phenotypes.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Ser. No. 09/456,100, filed Dec. 6, 1999, herein incorporated by reference in its entirety.

[0002] This application is related to U.S. Ser. No. 09/229,007, filed Jan. 12, 1999, and U.S. Ser. No. 09/229,037, filed Jan. 12, 1999, and U.S. Ser. No. 09/395,448, filed Sep. 14, 1999, herein each incorporated by reference in their entirety.

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Detail Description Paragraph - DETX (7):

[0039] In one embodiment, the zinc finger protein is linked to at least one

or more regulatory domains, described in detail below. Preferred regulatory domains include **transcription factor repressor or activat r** domains such as KRAB and VP16, co-repressor and co-activator domains, DNA **methyltransferases,** histone acetyltransferases, histone deacetylases, and endonucleases such as Fok1. For repression of gene expression, often simple steric hindrance of transcription initiation is sufficient.

Detail Description Paragraph - DETX (24):

[0056] A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (61):

[0093] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20020142981

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DOCUMENT-IDENTIFIER: US 20020142981 A1

TITLE: Gene expression profiles in liver cancer

PUBLICATION-DATE: October 3, 2002

INVENTOR-INFORMATION:

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APPL-NO: 09/ 880107

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US-CL-CURRENT: 514/44, 435/6

ABSTRACT:

The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

RELATED APPLICATIONS

[0001] This application is related to U.S. Provisional Application 60/211,379, filed on Jun. 14, 2000, and U.S. Provisional Application 60/237,054, filed Oct. 2, 2000, which are herein incorporated by reference in their entirety.

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Detail Description Table CWU - DETL (15):
9TABLE 6B Down in Metastatics vs Normal Sample Set 2 Fragment Name SEQ ID: Known Gene Name Fold Change Direction Pvalue N54417 2566 fibrinogen, A alpha polypeptide 99.28 down 0.00001 N53031 2555 UDP glycosyltransferase 2

family, polypeptide B4 97.58 down 0.00022 M15656 2268 aldolase B, fructose-bisphosphate 96.66 down 0 T73442 3212 EST 94.41 down 0 T59148 3157 carbamoyl-phosphate synthetase 1, mitochondrial 88.89 down 0 R49459 2881 transferrin receptor 2 85.61 down 0.00048 X55283 3731 asialoglycoprotein receptor 2 84.99 down 0.00084 cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), L16883 2166 polypeptide 9 84.71 down 0.00327 T48039 3128 protein C (inactivator of coagulation factors Va and VIIIa) 84.39 down 0.00112 T71373 3202 EST 83.08 down 0.00069 H58692 1960 formyltetrahydrofolate dehydrogenase 81.41 down 0 T46901 3122 EST 77.28 down 0.0006 M81349 2404 serum amyloid A4, constitutive 76.15 down 0.00015 R43174 2847 paraoxonase 1 74.04 down 0.00038 X65727 3765 glutathione S-transferase A2,glutathione S-transferase A3 73.64 down 0 M16594 2272 glutathione S-transferase A2 73.21 down 0 cytochrome P450, subfamily IIA (phenobarbital-inducible), U22029 3326 polypeptide 7 71.98 down 0 AA256367 579 paraoxonase 3 70.33 down 0.00192 cytochrome P450, subfamily IIA (phenobarbital-inducible), K03192 2127 polypeptide 6 69.92 down 0 AA035245 79 aldehyde oxidase 1 69.82 down 0.00117 N80129 2702 metallothionein 1L 66.48 down 0.00415 cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase), R97419 3003 polypeptide 1 65.07 down 0.0039 T83356 3231 apolipoprotein H (beta-2-glycoprotein I) 64.34 down 0.00802 fatty-acid-Coenzyme A ligase, long-chain 1,fatty-acid-Coenzyme A AA348922 758 ligase, long-chain 2 64.27 down 0.00002 T83397 3232 phytanoyl-CoA hydroxylase (Refsum disease) 63.6 down 0 R16098 2792 EST 63.41 down 0.00038 R89811 2979 HGF activator 62.51 down 0.00148 H57166 1955 EST 60.76 down 0.00007 N33009 2491 apolipoprotein E 60.54 down 0.0093 N54053 2560 secreted phosphoprotein 2, 24kD 60.39 down 0.00087 T68878 3190 carboxylesterase 1 (monocyte/macrophage serine esterase 1) 60.35 down 0.00409 R08564 2779 plasminogen-like 60.18 down 0.00091 F10182 1812 hepsin (transmembrane protease, serine 1) 58.92 down 0.00837 L25880 2184 epoxide hydrolase 1, microsomal (xenobiotic) 58.7 down 0.00013 W88946 3636 putative glycine-N-acyltransferase 58.26 down 0 N54429 2567 EST 57.81 down 0.00724 M29873 2318 cytochrome P450, subfamily IIB (phenobarbital-inducible) 56.71 down 0.0054 AA476324 1281 EST 55.22 down 0.00132 R12472 2788 EST 55.18 down 0.00011 AA453988 1160 methionine adenosyltransferase I, alpha 54.29 down 0.00381 T56264 3148 apolipoprotein C-II 53.04 down 0.00938 W92148 3647 kininogen 51.09 down 0.00376 R01023 2751 glucokinase (hexokinase 4) regulatory protein 50.71 down 0.00321 H80901 2005 ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen) 50.61 down 0.00262 D31628 1646 4-hydroxyphenylpyruvate dioxygenase 50.48 down 0.00002 AA401562 830 EST 50.45 down 0.00301 cytochrome P450, subfamily IIA (phenobarbital-inducible), K03192 2127 polypeptide 6 50.16 down 0 T67931 3183 fibrinogen, B beta polypeptide 49.55 down 0 M16974 2277 complement component 8, alpha polypeptide 49.47 down 0.00046 alcohol dehydrogenase 1 (class I), alpha polypeptide,alcohol dehydrogenase 2 (class I), beta polypeptide,alcohol dehydrogenase M12963 2248 3 (class I), gamma polypeptide 48.95 down 0.00104 T73433 3211 angiotensinogen 48.3 down 0.00049 AA009719 20 peroxisomal membrane protein 2 (22kD) 47.12 down 0.00008 H94666 2045 alpha-1-B glycoprotein 47.03 down 0.01158 T98676 3268 EST 46.94 down 0.0001 T40936 3117 EST 46.92 down 0.00056 R98073 3008 EST 46.87 down 0 AA456311 1190 EST 46.81 down 0.001 H91325 2029 aldolase B, frutose-bisphosphate 45.85 down 0.00505 H74317 1997 apolipoprotein A-II 45.09 down 0.01982 vitronectin (serum spreading factor, somatomedin B, complement S- T61373 3162 protein) 44.9 down 0.3172 X16260 3707 inter-alpha (globulin) inhibitor, H1 polypeptide 44.65 down 0.00933 AA421049 927 **activating transcription** factor 5 44.41 down

0.00179 M17262 2278 coagulation factor II (thrombin) 44.3 down 0.00345 cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18,cytochrome P450, subfamily IIC (mephenytoin 4- HG1827-HT1856 hydroxylase), polypeptide 8 44.17 down 0.0003 AA417046 915 fatty-acid-Coenzyme A ligase, very long-chain 1 44 down 0 AA433946 1033 EST 43.74 down 0.00005 T71012 3200 fibrinogen, B beta polypeptide 43.61 down 0.00743 L11244 2155 complement component 4-binding protein, beta 43.33 down 0 AA018867 39 EST 42.87 down 0.00002 T23882 3084 kininogen 42.85 down 0.00641 L00190 2130 antithrombin III 42.41 down 0.00012 N68596 2635 betaine-homocysteine **methyltransferase** 40.99 down 0 H94475 2043 alpha-2-plasmin inhibitor 40.92 down 0.00271 AA085987 183 UDP glycosyltransferase 1 40.87 down 0.00004 M75106 2396 carboxypeptidase B2 (plasma) 40.63 down 0 HG2841-HT2968 albumin 40.5 down 0.001 M58600 2362 heparin cofactor II 39.79 down 0.00034 R37128 2826 complement component 4A 39.51 down 0.00364 R93776 2992 EST 39.32 down 0.00176 cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), M61855 2371 polypeptide 9 38.82 down 0.00023 cytochrome P450, subfamily IIA (phenobarbital-inducible), X13930 3697 polypeptide 6 38.52 down 0 T95813 3261 KIAA1051 protein 38.38 down 0.00008 X68679 3776 complement factor H related 3,complement factor H-related 4 38.22 down 0.00036 W20094 3476 DKFZP586A0522 protein 38.09 down 0.00188 AA479148 1311 EST 38.05 down 0 AA235310 496 EST 37.86 down 0.00091 T68711 3187 EST 37.65 down 0.00036 R40395 2840 lecithin-cholesterol acyltransferase 37.33 down 0.00032 W28944 3493 EST 37.07 down 0.00205 U50929 3379 betaine-homocysteine **methyltransferase** 36.91 down 0 L04751 2138 cytochrome P450, subfamily IVA, polypeptide 11 36.79 down 0.00004 N76012 2693 EST 36.71 down 0.00598 T69284 3195 mannose-binding lectin (protein C) 2, soluble (opsonic defect) 36.53 down 0 R49602 2884 EST 36.5 down 0.00001 cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., - X07618 3688 metabolising), polypeptide 7a (pseudogene) 35.79 down 0.00065 N22938 2452 serum amyloid A4, constitutive 35.39 down 0.00128 AA621131 1513 EST 35.37 down 0 cytochrome P450, subfamily IVF, polypeptide 2,cytochrome P450, D12620 1601 subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase) 35.09 down 0.00015 N70358 2656 growth hormone receptor 34.35 down 0 solute carrier family 10 (sodium/bile acid cotransporter family), N70966 2662 member 1 34.06 down 0.0006 T68855 3188 EST 34.04 down 0 T69029 3193 haptoglobin 33.18 down 0.02825 cytochrome P450, subfamily IIA (phenobarbital-inducible)- , M33317 2338 polypeptide 7 32.63 down 0 T48075 3129 hemoglobin, alpha 1 32.56 down 0.00172 alcohol dehydrogenase 1 (class I), alpha polypeptide,alcohol dehydrogenase 2 (class I), beta polypeptide,alcohol dehydrogenase M12272 2243 3 (class I), gamma polypeptide 32.42 down 0.0034 AA620556 1505 EST 32.4 down 0.00353 T74542 3214 UDP glycosyltransferase 2 family, polypeptide B10 32.36 down 0.00004 T56281 3150 RNA helicase-related protein 32.34 down 0.00002 W73601 3589 EST 32.25 down 0 M11567 2239 angiogenin, ribonuclease, RNase A family, 5 32.25 down 0.0001 W86600 3625 EST 32.14 down 0 AA039335 89 coagulation factor XII (Hageman factor) 32 down 0.0029 T67705 3182 asialoglycoprotein receptor 2 31.6 down 0.00705 H89980 2026 protein phosphatase 1, regulatory (inhibitor) subunit 5 31.13 down 0.00006 H20543 1897 DKFZP586B1621 protein 31.03 down 0.00074 H57060 1954 EST 30.98 down 0.01687 W67564 3568 nuclear receptor subfamily 0, group B, member 2 30.34 down 0 N74422 2685 EST 30.32 down 0 X07173 3687 inter-alpha (globulin) inhibitor, H2 polypeptide 30.3 down 0.00016 T47778 3126 fibrinogen, A alpha polypeptide 30 down 0.01401 X90579 3816 EST 29.82 down 0.00273 T99636 3270 complement component 3 29.6 down 0.00051 Z20777 3863 EST 29.59 down 0.00044 U56814 3392 deoxyribonuclease I-like 3 29.43 down 0.00003

M19828 2287 apolipoprotein B (including Ag(x) antigen) 29.37 down 0.00137 R77628 2965 insulin induced gene 1 29.23 down 0.00122 AA452158 1141 ras homolog gene family, member B 28.96 down 0.00064 coagulation factor IX (plasma thromboplastic component, Christmas K02402 2125 disease, hemophilia B) 28.81 down 0.00001 T57140 3151 paraoxonase 3 28.8 down 0 T68873 3189 metallothionein 1L 28.72 down 0.02953 H95569 2051 DKFZP586A0522 protein 28.48 down 0.00139 T56279 3149 H factor (complement)-like 3 28.39 down 0.00016 N66066 2612 EST 28.35 down 0.00055

Detail Description Table CWU - DETL (35):

ribosomal protein S6 3.31 up 0.02144 R49395 2880 EST 3.31 up 0.00867 R53109 2898 dimethylarginine dimethylaminohydrolase 2 3.31 up 0.02406 AA485084 1340 EST 3.31 up 0.01232 AA136864 304 zinc finger protein homologous to Zfp-36 in mouse 3.31 up 0.00346 D31294 1643 EST 3.3 up 0.004 AA398141 788 EST 3.3 up 0.00211 AA465093 1267 TIA1 cytotoxic granule-associated RNA-binding protein 3.3 up 0.01314 H16251 1886 EST 3.3 up 0.03286 AA620761 1507 EST 3.3 up 0.00285 AA053662 129 EST 3.3 up 0.00558 M27830 2314 EST 3.3 up 0.02453 AF004022 1546 serine/threonine kinase 12 3.29 up 0.00841 AA476944 1288 EST 3.29 up 0.00189 AA452167 1142 EST 3.29 up 0.03337 T17339 3075 EST 3.29 up 0.00669 AA291644 701 EST 3.28 up 0.00033 Z47727 3937 polymerase (RNA) II (DNA directed) polypeptide K (7.0 kD) 3.28 up 0.00317 AA242757 522 EST 3.27 up 0.00286 AA458890 1206 EST 3.27 up 0.00079 R49482 2883 EST 3.27 up 0.0161 W42778 3510 EST 3.27 up 0.02411 AA022623 44 EST 3.27 up 0.01556 AA435662 1039 EST 3.27 up 0.0433 AA284565 675 EST 3.27 up 0.0362 N34825 2497 DKFZP434P106 protein 3.27 up 0.01334 H65030 1974 phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) 3.26 up 0.02278 Z40883 3921 EST 3.26 up 0.01863 AA621530 1526 EST 3.26 up 0.00298 AA091752 193 purine-rich element binding protein B 3.25 up 0.01419 AA092290 195 EST 3.25 up 0.01616 AA478971 1306 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein) 3.25 up 0.02698 AA610073 1497 EST 3.25 up 0.00859 AA251230 540 EST 3.25 up 0.01417 N64374 2607 KIAA0537 gene product 3.25 up 0.01652 W69468 3571 EST 3.25 up 0.00055 AA426374 964 tubulin, alpha 2 3.25 up 0.04346 D21063 1628 minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) 3.25 up 0.03558 AA598589 1431 EST 3.24 up 0.00432 R16144 2793 EST 3.24 up 0.0087 AA195067 414 GTPase activating protein-like 3.24 up 0.00606 W42788 3511 deoxynucleotidyltransferase, terminal 3.24 up 0.02261 U90426 3452 nuclear RNA helicase, DECD variant of DEAD box family 3.24 up 0.00035 AA279418 626 EST 3.23 up 0.02054 F04479 1789 KIAA1067 protein 3.23 up 0.04522 T94452 3256 EST 3.23 up 0.02245 W47206 3532 EST 3.23 up 0.01931 AA074162 159 superkiller viralicidic activity 2 (S. cerevisiae homolog)-like 3.23 up 0.00642 AA406384 875 KIAA0670 protein/acinus 3.23 up 0.00486 L06797 2143 chemokine (C-X-C motif), receptor 4 (fusin) 3.23 up 0.04782 T99312 3269 EST 3.22 up 0.00084 R54614 2901 EST 3.22 up 0.00334 D38305 1652 transducer of ERBB2, 1 3.22 up 0.0215 AA495857 1394 EST 3.21 up 0.02243 W28366 3488 EST 3.21 up 0.01007 AA465342 1271 EST 3.21 up 0.01378 M97856 2435 nuclear autoantigenic sperm protein (histone-binding) 3.21 up 0.00444 T10316 3051 EST 3.2 up 0.04794 AA429470 996 EST 3.2 up 0.0153 AA047704 120 EST 3.2 up 0.0029 AA132514 272 EST 3.2 up 0.00876 X14487 3699 keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) 3.19 up 0.01268 AA167708 363 EST 3.19 up 0.01871 AA431719 1025 EST 3.19 up 0.00294 AA070485 156 interleukin 13 receptor, alpha 1 3.19 up 0.03465 T47969 3127 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) 3.19 up 0.02283 M91083 2418

chromosome 11 open reading frame 13 3.19 up 0.00243 AA476754 1287 EST 3.18 up 0.01696 AA046410 110 EST 3.18 up 0.00797 AA131220 267 EST 3.18 up 0.00974 H73484 1995 ferritin, heavy polypeptide 1 3.18 up 0.00432 M61916 2372 laminin, beta 1 3.18 up 0.01171 AA453628 1154 EST 3.18 up 0.00849 AA465218 1268 DKFZP586M1523 protein 3.17 up 0.00357 N31597 2486 DKFZP564G2022 protein 3.17 up 0.03017 AA021549 42 EST 3.17 up 0.00158 AA025166 50 fusion, derived from t(12;16) malignant liposarcoma 3.17 up 0.00009 AA252524 555 EST 3.17 up 0.00686 W46810 3528 HMT1 (hnRNP **methyltransferase,** S. cerevisiae)-like 2 3.17 up 0.03434 AA045365 106 EST 3.17 up 0.0149 D57317 1688 **activated RNA polymerase II transcription** cofactor 4 3.17 up 0.00464 D80710 1734 integral type I protein 3.17 up 0.04549 AA296994 724 seven transmembrane domain protein 3.16 up 0.0076 AA256131 574 glycophosphatidylinositol anchor attachment 1 3.16 up 0.00011 AA282571 662 FSHD region gene 1 3.16 up 0.01355 AA321833 736 EST 3.16 up 0.00523 AA430675 1019 Fanconi anemia, complementation group G 3.16 up 0.01007 AA235853 503 CGI-96 protein 3.16 up 0.00744 N93316 2732 EST 3.16 up 0.01262 R51908 2891 EST 3.16 up 0.0083 AA136474 301 Meis (mouse) homolog 2 3.15 up 0.02837 AA463934 1253 splicing factor 3b, subunit 4, 49 kD 3.15 up 0.00952 W56642 3544 EST 3.15 up 0.00654 AA070206 155 EST 3.15 up 0.03914 AA251428 542 DKFZP586I2223 protein 3.15 up 0.01223 AA253011 558 KIAA0713 protein 3.15 up 0.00035 AA258387 594 EST 3.15 up 0.02028 AA621146 1514 MUF1 protein 3.15 up 0.02116 N69879 2650 drebrin 1 3.15 up 0.01659 AA047379 119 karyopherin (importin) beta 1 3.15 up 0.01572 AA398563 797 EST 3.14 up 0.01895 AA478415 1299 EST 3.14 up 0.0483 U18321 3317 death associated protein 3 3.14 up 0.00833 AA482319 1335 putative type II membrane protein 3.13 up 0.00071 AA086412 187 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 3.13 up 0.00327 AA256268 576 EST 3.13 up 0.03874 AA450247 1133 EST 3.13 up 0.00531 AA621752 1529 26S proteasome-associated pad1 homolog 3.13 up 0.01571 D20899 1626 EST 3.13 up 0.02128 H89987 2027 ATP-binding cassette, sub-family C (CFTR/MRP), member 5 3.13 up 0.01194 N90238 2711 EST 3.13 up 0.02492 R39610 2837 calpain, large polypeptide L2 3.13 up 0.01863 X14850 3703 H2A histone family, member X 3.13 up 0.01523 Y08999 3852 actin related protein 2/3 complex, subunit 1A (41 kD) 3.13 up 0.02376 HG2994-HT4850 elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) 3.13 up 0.01206 AA446570 1089 EST 3.12 up 0.02228 D13636 1606 general transcription factor IIIC, polypeptide 2 (beta subunit, 110 kD) 3.12 up 0.00022 L34587 2200 transcription elongation factor B (SIII), polypeptide 1 (15 kD, elongin C) 3.12 up 0.00946 S67070 3022 heat shock 27 kD protein 2 3.12 up 0.01688 U59321 3397 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72 kD) 3.12 up 0.02469 AA429825 1003 DKFZP566B023 protein 3.11 up 0.01857 W49743 3537 EST 3.11 up 0.01121 N69084 2642 EST 3.11 up 0.0094 AA236412 511 EST 3.1 up 0.04463 W02695 3466 EST 3.1 up 0.04745 AA285132 682 apoptotic protease activating factor 3.1 up 0.00844 AA621367 1523 EST 3.1 up 0.00066 H48459 1937 KIAA0186 gene product 3.1 up 0.02325 N53067 2556 DKFZP547E1010 protein 3.1 up 0.00101 X92896 3826 DNA segment on chromosome X (unique) 9879 expressed sequence 3.1 up 0.0405 AA005262 13 EST 3.09 up 0.0064 AA430154 1014 EST 3.09 up 0.04401 AA433947 1034 EST 3.09 up 0.00253 AA599808 1455 EST 3.09 up 0.00726 Z38431 3886 EST 3.09 up 0.0083 AA405544 861 EST 3.09 up 0.04146 AA446970 1098 EST 3.09 up 0.01627 D80917 1736 KIAA0670 protein/acinus 3.09 up 0.00168 W72187 3579 EST 3.09 up 0.00134 AA478615 1305 H1 histone family, member X 3.09 up 0.0499 W15495 3473 chromosome 21 open reading frame 5 3.09 up 0.00491 W58247 3548 kinesin family member 4 3.08 up 0.00048 AA428204 987 cofactor required for Sp1 transcriptional activation, subunit 6 (77 kD) 3.08 up 0.00313 AA481060 1326 EST 3.08 up 0.00029 AA481420 1327 EST 3.08 up

0.0206 AA505141 1418 EST 3.08 up 0.02327 T41078 3120 bromodomain adjacent to zinc finger domain, 2B 3.08 up 0.03426 N29484 2477 EST 3.08 up 0.04834 R60512 2917 KIAA0191 protein 3.08 up 0.00856 AA011679 32 EST 3.08 up 0.03649 AA427734 977 cholinergic receptor, nicotinic, epsilon polypeptide 3.08 up 0.04796 D86957 1754 KIAA0202 protein 3.08 up 0.02949 M86667 2410 nucleosome assembly protein 1-like 1 3.08 up 0.00473 AA031814 70 KIAA0958 protein 3.07 up 0.00681 AA236904 518 EST 3.07 up 0.01503 D80946 1737 SFRS protein kinase 1 3.07 up 0.00986 W42674 3509 EST 3.07 up 0.0261 W74536 3595 advanced glycosylation end product-specific receptor 3.07 up 0.00251 AA435681 1041 EST 3.07 up 0.01166 AA599469 1450 EST 3.07 up 0.04154 D13370 1603 APEX nuclease (multifunctional DNA repair enzyme) 3.07 up 0.00857 HG4297-HT4567 activated RNA polymerase II transcription cofactor 4 3.07 up 0.00787 M93036 2421 membrane component, chromosomal 4, surface marker (35 kD glycoprotein) 3.07 up

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TITLE: Methods for altering cell fate

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INVENTOR-INFORMATION:

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US-CL-CURRENT: 435/69.5, 435/320.1 , 435/325 , 435/455

ABSTRACT:

The invention provides methods for altering the expression profile of a cell to convert the cell from one cell type to a desired cell type. These reprogrammed cells may be used in a variety of medical applications for treating a mammal in need of a particular cell type.

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of the filing date of U.S. provisional application No. 60/258,152, filed Dec. 22, 2000.

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Summary of Invention Paragraph - BSTX (22):

[0021] In still other preferred embodiments, the reprogramming media is an interphase reprogramming media, such as an extract formed from cells synchronized in one or more of the following phases of the cell cycle: G.sub.0, G.sub.1, S, or G.sub.2 phase. In another preferred embodiment, the reprogramming media is an extract formed from cells synchronized in mitosis or from unsynchronized cells. Preferably, the reprogramming media is an extract from the cell type one wishes the donor or permeabilized cell to become, or the reprogramming media is a solution containing factors specific for the cell type one wishes the donor or permeabilized cell to become. Examples of cells that

may be used to generate extracts to reprogram cells into stem cells include embryonic stem cells and adult stem cells from brain, blood, bone marrow, pancreas, liver, skin, or any other organ or tissue. Preferably, the donor or permeabilized cell is an interphase or mitotic somatic cell. In another preferred embodiment, the reprogramming media is modified by the enrichment or depletion of a factor, such as a DNA **methyltransferase,** histone deacetylase, histone, nuclear lamin, **transcription factor, activator,** repressor, growth factor, hormone, or cytokine. The reprogramming media may or may not contain exogenous nucleotides. In other preferred embodiments, a chromatin mass in a reprogramming media or formed in a permeabilized cell is contacted with a vector having a nucleic acid encoding a gene of interest under conditions that allow homologous recombination between the nucleic acid in the vector and the corresponding nucleic acid in the genome of the chromatin mass, resulting in the alteration of the genome of the chromatin mass. Due to the lack of an intact plasma membrane and the lack of a nuclear membrane, a chromatin mass in a permeabilized cell may be easier to genetically modify than a naturally-occuring cell. Preferably, the chromatin mass or nucleus is purified from the reprogramming media prior to insertion into the recipient cell or cytoplast, or the reprogrammed cell is purified prior to administration into the mammal. Preferably, the donor or permeabilized cell is haploid (DNA content of n), diploid (2n), or tetraploid (4n), and the recipient cell is hypodiploid (DNA content of less than 2n), haploid, or enucleated.

Summary of Invention Paragraph - BSTX (35):

[0034] Exemplary reprogramming medias include solutions, such as buffers, that do not contain biological molecules such as proteins or nucleic acids. Such solutions are useful for the removal of one or more factors from a nucleus, chromatin mass, or chromosome. Other preferred reprogramming medias are extracts, such as cellular extracts from cell nuclei, cell cytoplasm, or a combination thereof. Yet other reprogramming medias are solutions or extracts to which one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, nuclear lamins, **transcription factors, activators,** repressors, growth factors, hormones, or cytokines) have been added, or extracts from which one or more factors have been removed. Still other reprogramming medias include detergent and salt solutions and protein kinase solutions. In some embodiments, the reprogramming media contains an anti-NuMA antibody. By "interphase reprogramming media" is meant a media (e.g., an interphase cell extract) that induces chromatin decondensation and nuclear envelope formation. By "mitotic reprogramming media" is meant a media (e.g., a mitotic cell extract) that induces chromatin condensation and nuclear envelope breakdown. If desired, multiple reprogramming media may be used simultaneously or sequentially to reprogram a donor cell, nucleus, or chromatin mass.

Summary of Invention Paragraph - BSTX (38):

[0037] By "enrichment or depletion of a factor" is meant the addition or removal of a naturally-occurring or recombinant factor by at least 20, 40, 60, 80, or 100% of the amount of the factor originally present in the reprogramming media. Alternatively, a naturally-occurring or recombinant factor that is not naturally present in the reprogramming media may be added. Preferred factors include proteins such as DNA **methyltransferases,** histone deacetylases,

histones, nuclear lamins, **transcription factors, activators,** repressors, growth factors, cytokines, and hormones; membrane vesicles; and

Detail Description Paragraph - DETX (13):

[0111] These methods are described further below. It is noted that any of the methods described below can be performed with reprogramming media other than cell extracts. For example, a reprogramming media can be formed by adding one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, nuclear lamins, **transcription factors, activators,** repressors, growth factors, hormones, or cytokines) to a solution, such as a buffer. Preferably, one or more of the factors are specific for the cell type one wishes the donor cell to become.

Detail Description Paragraph - DETX (28):

[0124] As an alternative to a cell extract, a reprogramming media can also be formed by adding one or more naturally-occurring or recombinant factors (e.g., nucleic acids or proteins such as DNA **methyltransferases,** histone deacetylases, histones, nuclear lamins, **transcription factors, activators,** repressors, growth factors, hormones, or cytokines) to a solution, such as a buffer. Preferably, one or more of the factors are specific for the cell type one wishes the donor cell to become.

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INVENTOR-INFORMATION:

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ABSTRACT:

The invention provides isolated nucleic acid molecules, designated TPRM nucleic acid molecules, which encode novel methyltransferase family members. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing TPRM nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a TPRM gene has been introduced or disrupted. The invention still further provides isolated TPRM proteins, fusion proteins, antigenic peptides and anti-TPRM antibodies. Diagnostic and therapeutic methods utilizing compositions of the invention are also provided.

RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Application Serial No. 60/227,867, filed Aug. 24, 2000, the entire contents of which are incorporated herein by this reference.

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Summary of Invention Paragraph - BSTX (7):
[0007] One type of protein methylation is mediated by **arginine**

methyltransferases. One subtype of **arginine methyltransferase,** the type I **arginine methyltransferases,** catalyze the formation of monomethylarginine and asymmetric NG,NG-dimethylarginine in a variety of substrates (Tang, J. et al. (2000) J. Biol. Chem. 275:19866-19876), including many RNA-binding proteins (Najbauer, J. et al. (1993) J. Biol. Chem. 268:10501-10509), RNA-transporting proteins (Najbauer et al. (1993) supra), transcription factors (Gary, J. D. and Clarke, S. (1998) Prog. Nucleic Acids Res. Mol Biol. 61:65-131; Chen, D. et al. (1999) Science 284:2174-2177), nuclear matrix proteins (Gary and Clarke (1998) supra), and cytokines (Sommer, A. et al. (1989) Biochem. Biophys. Res. Commun. 160:1267-1274). Methylation by type I **arginine methyltransferases** modifies the activities of transcription factors (Gary and Clarke (1998) supra), modulates the affinity of nucleic acid binding proteins for nucleic acids (Gary and Clarke (1998) supra), regulates interferon signaling pathways (Abramovich, C. et al. (1997) EMBO J. 16:260-266), and alters targeting of nuclear proteins (Pintucci, G. et al. (1996) Mol. Biol. Cell 7:1249-1258).

Brief Description of Drawings Paragraph - DRTX (4):

[0020] FIGS. 3A-3E depict an alignment of the human TPRM amino acid sequence with the amino acid sequences of known methyltransferases. The alignment was made using the program MegAlign, using the Clustal method with PAM250 residue weight table. Amino acid residues identical to the TPRM amino acid sequence are boxed. The location of the MT I, MT II, and MTIII motifs are underlined. The aligned sequences are as follows: mouse **arginine methyltransferase** (Prmt2; GenBank Accession No. AF169620; SEQ ID NO:7); human protein arginine N-methyltransferase 1-variant 1 (HRMT1L2; GenBank Accession Nos. AF222689 or AAF62895; SEQ ID NO:8); mouse protein arginine N-methyltransferase 1 (Mrmt1; GenBank Accession No. AF232716; SEQ ID NO:9); Arabidopsis thaliana **arginine methyltransferase** (pam1; GenBank Accession Nos. AL079344 or CAB45311; SEQ ID NO:10); yeast HNRNP Arginine N-Methyltransferase (Odp1; GenBank Accession No. P38074; SEQ ID NO:11); rat Protein Arginine N-Methyltransferase 1 (GenBank Accession No. Q63009; SEQ ID NO:12).

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INVENTOR-INFORMATION:

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ABSTRACT:

Novel proteins IR1B1 and IR1B4 have been isolated which bind to the type I IFN receptor IFNAR1 and function in the cellular response to IFNs. DNA encoding such proteins in either the sense or anti-sense orientation can be administered to either enhance or inhibit the cellular response to IFNs. Antibodies to the proteins can be used for isolation of the new protein or for immunodetection thereof.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a division of U.S. application Ser. No. 09/341,650, filed Oct. 8, 1999, which is the national stage under 35 U.S.C. 371 of PCT/US98/00671, filed Jan. 15, 1998, which international application claims the benefit under 35 U.S.C. .sctn.119(e) of U.S. provisional

application No. 60/035,636, filed Jan. 15, 1997, now abandoned.

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Brief Description of Drawings Paragraph - DRTX (12):

[0023] FIG. 11 shows an assay of protein-argintne methyltransferase activity in U266S cells. In lane 1, the protein-**arginine methyltransferase** activity of human U266S cells was measured by methylation of peptide R1, having the sequence of SEQ ID NO:11. In lane 2 an anti-sense oligonucleotide of SEQ ID NO:12, complementary to the sequence of nucleotides 12-33 around the initiation codon of IR1B4 cDNA, was added. In lane 3 the corresponding sense oligonucleotide was added. It is seen that the anti-sense oligonucleotide substantially inhibits the protein-**arginine methyltransferase** activity while the control sense oligonucleotide has little effect.

Detail Description Paragraph - DETX (5):

[0028] While IR1B4, like IR1B1, was found to be a novel protein as determined by computer searches of sequence databases, it was also found that IR1B4 has sequence homology to enzymes which utilize S-adenosyl methionine for methylating arginine residues in proteins and are designated as protein **arginine methyltransferases** (PRMT1; Kagan and Clarke, 1994; Lin et al, 1996). IR1B4 was found to bind directly to the IC-domain of IFNAR1 in vitro, and the constitutive association of PRMT activity with the IFNAR chain of the IFN-.alpha., .beta. receptor isolated from human cells was demonstrated by methylation of histones. When anti-sense oligodeoxynucleotides from the IR1B4 cDNA was added to human cell cultures, depletion of PRMT activity in the cell culture was observed. Human myeloma cells that were treated in this manner showed a much reduced response to IFN as measured by growth-inhibition. Therefore, IR1B4/PRMT is involved in the pathway by which the IFN receptor causes growth-inhibition in tumor cells and is also involved in other functions of the IFN receptor. Known substrates of PRMT include a number of RNA and DNA binding proteins, and in particular heterologous nuclear ribonucleoproteins (hnRNPs). The hnRNPs are involved in mRNA transport from the nucleus to the cytoplasm, alternative splicing of pre-mRNA, and post-transcriptional controls (Liu and Dreyfuss, 1995). Accordingly, the novel human IR1B4/PRMT cDNA and protein, which were discovered by its association with the IFN receptor, can be used to modify the response of human or animal cells to IFN.

Detail Description Paragraph - DETX (15):

[0038] The anti-sense sequence need not hybridize to the entire length of the IR1B1 or IR1B4 mRNA. Instead, it may hybridize to selected regions, such as the 5'-untranslated non-coding sequence, the coding sequence, or the 3'-untranslated sequence of the "sense" mRNA. Preferably, the anti-sense sequence hybridizes to the 5'-coding sequence and/or 5'-non-coding region, such as at cap and initiation codon sites, since it has been observed it has been observed with many examples of anti-sense oligonucleotides that targeting the initiation codon is more effective, whereas targeting internal sequences within the coding region is not as effective (Wickstrom, 1991). The effectiveness of an anti-sense sequence in preventing translation of IR1B4 sense mRNA can easily

be tested in an assay for protein-**arginine methyltransferase** activity in U266S cells as described in Example 7. In view of the size of the mammalian genome, the anti-sense IR1B1 or IR1B4 sequence is preferably at least 17, more preferably at least 30 base pairs in length. However, shorter sequences may still be useful, i.e., they either fortuitously do not hybridize to other mammalian sequences, or such "cross-hybridization" does not interfere with the metabolism of the cell in a manner and to a degree which prevents the accomplishment of the objects of this invention.

Detail Description Paragraph - DETX (57):

[0075] The nucleotide sequence of the IR1B4 cDNA has an open reading frame encoding a 361 amino-acid long protein (FIG. 7). This human cDNA recognized a 1.5 kb constitutively expressed poly-A.sup.+ mRNA in various human cells including U266 myeloma cells. An online search of the protein databases was performed using the BlastP algorithm (Altschul et al, 1990) as well as the Bioaccelerator Alignment (Henikoff and Henikoff, 1992), and it was found that IR1B4 is a unique member of the protein-**arginine methyltransferase** family. The rat PRMT1 cDNA described by Lin et al (1996, Genbank sequence I.D. 1390024; Accession U60882) is only 81.4% homologous when analyzed by the ALIGN computer program. At the amino acid level (FIG. 8), the human IR1B4/PRMT differs clearly in its amino terminus from PRMT1, with the first 19 amino acids being completely different. N-terminal sequencing of IR1B4 alone would not have provided any indication that IR1B4 is homologous to PRMT1. Another human protein which has been described, HCP-1 (Nikawa et al, 1996; Genbank accession D66904) was also found to have homology to IR1B4. However, HCP-1 has a different amino acid sequence from residues 147-175 (FIG. 9). HCP-1 was originally identified based on its ability to complement the ire15 mutation in yeast and its enzymatic function was not previously identified (Nikawa et al, 1996). Therefore, IR1B4 is a novel human protein.

Detail Description Paragraph - DETX (63):

[0079] An anti-sense oligodeoxynucleotide phosphorothioate (Stein et al, 1989) complementary to the sequence of nucleotides 12-33 around the initiation codon of IR1B4 cDNA (AS-1, anti-sense sequence 5'TGGCTACAAAATTCTCCATGATG-3'; SEQ ID NO:12) was synthesized chemically. The oligonucleotides were added to U266S cells seeded in 96-well microplates (8000 cells/well/0.2 ml RPMI, 10% FCS) at a final concentration of 10 .mu.M on day 0 and re-added at 5 .mu.M on day 2. IFN-.beta. was added at 64 or 125 IU/ml on day 0. After 3 days of culture, 20 .mu.l of Alamar Blue, a colorimetric cell density indicator based on oxido-reduction (BioSource, Camarillo, Calif.), was added to each well and incubation continued for 6-7 h. Color was measured in a microplate ELISA reader (test filter 530 nm, reference filter 630 nm) with multiple reading of duplicate wells. Correlation of the growth curves by live cell number and by OD was verified. To measure methyltransferase, cells from pooled wells were lysed by freeze-thawing in 25 .mu.l/well of 25 mM Tris-HCl, pH 7.4, 1 mM EDTA, 1 mM EGTA, 40 .mu.g/ml leupeptin and aprotinin, 20 .mu.g/ml pepstatin, 1 UM phenylmethylsulfonyl fluoride (PMSF). Reactions were in 50 .mu.l with 25 .mu.l of cell extracts, 100 .mu.M peptide R1 (Najbauer et al, 1993; obtained from Genosys, Cambridge, UK), 3 .mu.Ci of [.sup.3H](methyl)S-adenosylmethionine (Amersham, 73 Ci/mmol) for 30 min at 30.degree. C. After electrophoresis in SDS-polyacrylamide (16%) gel, fixation in 50% methanol, 10% acetic acid and

treatment by Amplify (Amersham), autoradiography was carried out for 8 days. This AS-1 anti-sense DNA was able to strongly reduce the protein-**arginine methyltransferase** activity in U266S cells as measured by incorporation of tritiated-methyl groups to the R1 peptide substrate (FIG. 11), and was used to investigate the role that this enzyme may play in IFN action. The growth-inhibitory activity of IFN was chosen because it can be most directly quantified on cells and because an interaction of rat PRMT1 with growth-related gene products has been observed (Lin et al, 1996). Addition of the antisense-I oligonucleotide AS-1, which is complementary to the sequence around the initiation codon of IR1B4/PRMT cDNA, reduced the growth inhibitory effect of IFN-.beta. on human myeloma U266S cells (FIG. 12). This means that, in the presence of anti-sense AS-1, the IFN-treated cells exhibited a higher growth (excluding any toxic effect of phosphorothioates). The growth in the absence of IFN was not significantly affected. The sense oligonucleotide S-3 corresponding to the same cDNA region had only a small effect (S-3, FIG. 12) as compared to antisense-I. Sense S-3 also had only a slight inhibitory effect on the level of enzyme activity (FIG. 11). Another anti-sense phosphorothioate oligonucleotide AS-2 (SEQ ID NO:13), directed to the middle of the cDNA and complementary to nucleotides 572-592 of SEQ ID NO:7, had almost no effect (FIG. 12). The up to 5 fold reduction in the growth inhibitory effect of IFN-.beta. on myeloma cells, which were rendered partially deficient in PRMT activity by antisense-I oligonucleotide demonstrates that the association of the IR1B4/PRMT enzyme with the IC domain of the IFNAR1 receptor is functionally significant for IFN action on cells.

Detail Description Paragraph - DETX (95):

[0110] Lin et al, "The mammalian immediate-early TIS21 protein and the leukemia-associated BTG1 protein interact with a Protein-**arginine Methyltransferase**", J Biol Chem 271:15034-15044 (1996)

PGPUB-DOCUMENT-NUMBER: 20020115629

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020115629 A1

TITLE: Aptamer-mediated regulation of gene expression

PUBLICATION-DATE: August 22, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 10/ 036091

DATE FILED: October 19, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60242106 20001020 US

US-CL-CURRENT: 514/44, 536/23.1

ABSTRACT:

This invention provides methods of regulating gene expression. An aptamer is positioned in a nucleic acid molecule along with a sequence encoding a transcriptional regulatory polypeptide. The aptamer disrupts translation of the transcriptional regulatory polypeptide when contacted with an aptamer-binding ligand. Gene expression levels can be either increased or decreased by the disclosed methods, depending on whether the transcriptional regulatory polypeptide is a repressor or activator, and the degree of the effect is dependent upon the dose of the ligand. Nucleic acid molecules, expression cassettes, expression vectors and cells useful in the gene regulation methods are also provided.

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Application No. 60/242,106, filed Oct. 20, 2000, which application is incorporated herein by reference for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (19):
[0029] "transcriptional regulatory polypeptide" refers to a protein or effector domain of protein that has the ability to modulate transcription. A transcriptional regulatory polypeptide may act as either a **transcripti nal**

activator, a transcripti nal repressor, or in some rare cases, as either. Transcriptional regulatory polypeptides include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP 16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

PGPUB-DOCUMENT-NUMBER: 20020115215

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020115215 A1

TITLE: Targeted modification of chromatin structure

PUBLICATION-DATE: August 22, 2002

INVENTOR-INFORMATION:

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APPL-NO: 09/ 844508

DATE FILED: April 27, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60200590 20000428 US

non-provisional-of-provisional 60228523 20000828 US

US-CL-CURRENT: 435/455, 435/468 , 435/6

ABSTRACT:

Methods and compositions for targeted modification of chromatin structure, within a region of interest in cellular chromatin, are provided. Such methods and compositions are useful for facilitating processes such as, for example, transcription and recombination, that require access of exogenous molecules to chromosomal DNA sequences.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority under the provisions of 35 U.S.C. .sctn.119 to U.S. Provisional Patent Application Serial No. 60/200,590, filed Apr. 28, 2000 and U.S. Provisional Patent Application Serial No. 60/228,523, filed Aug. 28, 2000; the disclosures of which are hereby incorporated by reference in their entireties.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (9):

[0008] A number of enzymes capable of chemical modification of histones have been described and partially characterized. For example, histone acetyl transferases include Gcn5p, p300/CBP-associated factor (P/CAF), p300,

CREB-binding protein (CBP), HAT1, TFIID-associated factor 250 (TAF.sub.II250), and **steroid receptor** coactivator-1 (SRC-1). Wade et al. (1997) Trends Biochem. Sci. 22:128-132; Kouzarides (1999) Curr. Opin. Genet. Devel. 9:40-48; Sterner et al. (2000) Microbiol. Mol. Biol. Rev. 64:435-459. The HDAC family of proteins have been identified as histone deacetylases and include homologues to the budding yeast histone deacetylase RPD3 (e.g., HDAC1, HDAC2, HDAC3 and HDAC8) and homologues to the budding yeast histone deacetylase HDA1 (e.g., HDAC4, HDAC5, HDAC6 and HDAC7). Ng et al. (2000) Trends Biochem. Sci. 25:121-126. The Rsk-2 (RKS90) kinase has been identified as a histone kinase. Sassone-Corsi et al. (1999) Science 285:886-891. A histone **methyltransferase** (CARM-1) has also been identified. Chen et al. (1999) Science 284:2174-2177.

PGPUB-DOCUMENT-NUMBER: 20020110563

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020110563 A1

TITLE: Compositions and methods for the therapy and diagnosis of lung cancer

PUBLICATION-DATE: August 15, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 738973

DATE FILED: December 14, 2000

RELATED-US-APPL-DATA:

child 09738973 A1 20001214

parent continuation-in-part-of 09704512 20001101 US PENDING

US-CL-CURRENT: 424/155.1, 435/183 , 435/320.1 , 435/325 , 435/6 , 435/69.1 , 435/7.23 , 536/23.1

ABSTRACT:

Compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compositions comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is related to U.S. patent application Ser. No. 09/704,512, filed Nov. 1, 2000; U.S. patent application Ser. No. _____, filed Sep. 20, 2000; U.S. patent application Ser. No. 09/640,878, filed Aug. 18, 2000; U.S. patent application Ser. No. 09/588,937, filed Jun. 5, 2000; U.S. patent application Ser. No. 09/538,037, filed Mar. 29, 2000; U.S. patent application Ser. No. 09/518,809, filed Mar. 3, 2000; U.S. patent application Ser. No. 09/476,235 filed Dec. 30, 1999; U.S. patent application Ser. No. 09/370,838, filed Aug. 9, 1999; and U.S. patent application Ser. No. 09/285,323, filed Apr. 2, 1999, each a CIP of the previous application and all pending, and PCT/US00/08560, filed Mar. 30, 2000, pending.

--------- KWIC ---------

Detail Description Table CWU - DETL (3):

4TABLE 4 SEQ GenBank Clone ID NO: Accession Description 55163 458, 459 Novel in Genbank 55158 452 Novel in Genbank Homology to known sequences with unknown function 55153 443, 444 7018516 H. sapiens mRNA; cDNA DKFZp434M035 55154 445, 446 6437562 H. sapiens Chr 22q11 PAC Clone p393 55157 450, 451 2887408 H. sapiens K1AA0417 mRNA 55165 462, 463 3970871 H. sapiens HRIHFB2122 mRNA Homology to known sequences with known function 55155 447 7677405 H. sapiens F-box protein FBS (FBS) 55156 448, 449 3929584 H. sapiens EEN pseudogene 55161 454, 455 4503350 H. sapiens DNA (cytosine-5-)-**methyltransferase** 1 (DNMT1) 55162 456, 457 31220 ERK1 mRNA for protein serine/ threonine kinase 55164 460, 461 6677666 H. sapiens RNA-binding protein (autoantigenic) (RALY) 55166 464, 465 3249540 H. sapiens ribonuclease P protein subunit p40 (RPP40) 55167 466, 467 7657497 H. sapiens renal tumor antigen (RAGE) 55168 468, 469 2873376 H. sapiens exportin t mRNA 55169 470, 471 3135472 H. sapiens Cre binding protein-like 2 mRNA 55171 474 4759151 H. sapiens spermine synthase (SMS) 55173 476 6688148 H. sapiens partial mRNA for NICE-3 protein 55174 477, 478 531394 Human **transcriptional coactivator** PC4 55175 479 6563201 H. sapiens translation initiation factor eIF-2b delta subunit 55176 480 29860 hCENP-Bgene, for centromere autoantigen B (CENP-B) Homology to Ribosomal Protein 55159 453 337494 Ribosomal protein L7a (surf 3) large subunit mRNA 55170 472, 473 4506648 H. sapiens mRNA for ribosomal protein L3 55172 475 388031 H. sapiens ribosomal protein L11

PGPUB-DOCUMENT-NUMBER: 20020107376

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020107376 A1

TITLE: 26199, 33530, 33949, 47148, 50226, and 58764, novel human transferase family members and uses therefor

PUBLICATION-DATE: August 8, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Meyers, Rachel	Newton	MA	US	
MacBeth, Kyle	Boston	MA	US	

APPL-NO: 09/ 924358

DATE FILED: August 6, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60229300 20000901 US

US-CL-CURRENT: 536/23.2, 435/193 , 435/320.1 , 435/325 , 435/6 , 435/69.1 , 435/7.23

ABSTRACT:

The invention provides isolated nucleic acids molecules, designated 26199, 33530, 33949, 47148, 50226, or 58764 nucleic acid molecules, which encode novel transferase family members. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing 26199, 33530, 33949, 47148, 50226, or 58764 nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 26199, 33530, 33949, 47148, 50226, or 58764 gene has been introduced or disrupted. The invention still further provides isolated 26199, 33530, 33949, 47148, 50226, or 58764 proteins, fusion proteins, antigenic peptides and anti-26199, -33530, -33949, -47148, -50226, or -58764 antibodies. Diagnostic methods utilizing compositions of the invention are also provided.

[0001] This application claims priority on U.S. Application Serial No. 60/229,300 filed Sep. 1, 2000, which is relied on and incorporated herein by reference in its entirety.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (12):

[0012] Protein **arginine methyltransferases** transfer a methyl group from

S-adenosylmethionine to the guanidino group nitrogen atoms in arginine residues of specific proteins. The enzyme modifies a number of generally nuclear or nucleolar protein substrates in vitro, including histones and proteins involved in RNA metabolism such as hnRNPA1, fibrillarin, and nucleolin. Roles for protein methylation in transcription regulation and in cancer cell proliferation are mentioned below.

Summary of Invention Paragraph - BSTX (13):

[0013] A mouse **arginine methyltransferase** (CARMI) has been identified and shown to enhance the **transcriptional activation** by nuclear hormone receptors, suggesting that methylation of proteins in the transcription machinery may affect transcription regulation of nuclear receptor-mediated gene expression. Chen, D., et al, 1999, Regulation of transcription by a protein **methyltransferase**. Science, 284:2174-2177.

Detail Description Paragraph - DETX (13):

[0080] In one embodiment, a 26199 family member can include at least one and preferably two transmembrane domains. Furthermore, a 26199 family member can include at least one and preferably two glycosaminoglycan attachment sites (PS00002); at least one cAMP- and cGMP-dependent protein kinase phosphorylation site (PS00004); at least one, and preferably two protein kinase C phosphorylation sites (PS00005); at least one, two, three, four, five, and preferably six casein kinase II phosphorylation sites (PS00006); at least one, two, three, and preferably four N-myristolyation sites (PS00008); at least one prokaryotic membrane lipoprotein lipid attachment site (PS00013). 26199 is overexpressed in human breast and lung carcinomas. It is expected that inhibition of this **arginine methyltransferase** will inhibit tumor progression.

PGPUB-DOCUMENT-NUMBER: 20020106735

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020106735 A1

TITLE: Novel Bcl-2 related proline rich protein (BPR)

PUBLICATION-DATE: August 8, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Scorilas, Andreas	Athens		GR	
Diamandis, Eleftherios	Toronto		CA	

APPL-NO: 09/ 953342

DATE FILED: September 14, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60233026 20000915 US

US-CL-CURRENT: 435/69.1, 435/320.1 , 435/325 , 530/350 , 536/23.5

ABSTRACT:

The invention relates to nucleic acid molecules, proteins encoded by such nucleic acid molecules; and use of the proteins and nucleic acid molecules.

---------- KWIC ---------

Detail Description Paragraph - DETX (184):

[0226] The new gene is localized in an area that contains a number of well studied genes such as the RRAS, IRF3 and PRMT1/HRMT1L2. The RRAS gene encodes a small GTPase (41,42). Although its function is not fully understood, it has been shown to promote integrin activity and cell adhesion (19, 43). The IRF3 gene encodes a protein which binds to the interferon stimulated response element and activates expression of interferon-stimulated genes (44,45). The PRMT1 gene encodes an **arginine methyltransferase** which has been shown to reduce the antiproliferative effect of interferon (46, 47). The apoptosis regulator gene BAX is also located in chromosome 19q13.3 (48, 49). These genes have been shown to be involved in malignancy, directly (e.g. RRAS) or indirectly.

Detail Description Paragraph - DETX (237):

[0278] 46. Scott, H. S., Antonarakis, S. E., Lalioti, M. D., Rossier, C., Silver, P. A., and Henry, M. F. Identification and characterization of two putative human **arginine methyltransferases** (HRMT1L1 and HRMT1L2). Genomics.

48: 330-40, 1998.

Detail Description Paragraph - DETX (238):
[0279] 47. Abramovich, C., Yakobson, B., Chebath, J., and Revel, M. A protein-**arginine methyltransferase** binds to the intracytoplasmic domain of the IFNAR1 chain in the type I interferon receptor. Embo J. 16: 260-6, 1997.

PGPUB-DOCUMENT-NUMBER: 20020094529

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020094529 A1

TITLE: Gene identification

PUBLICATION-DATE: July 18, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 941450

DATE FILED: August 28, 2001

RELATED-US-APPL-DATA:

child 09941450 A1 20010828

parent continuation-in-part-of 09395448 19990914 US PENDING

US-CL-CURRENT: 435/6, 435/4 , 435/455

ABSTRACT:

The present disclosure provides methods and compositions for identifying a particular genomic sequence as a gene and/or a coding region, once that sequence has been tentatively identified as a gene based on genomic analysis using one or more gene prediction algorithms. The methods include the use of exogenous molecules such as zinc finger proteins which are capable of binding to and modulating expression of gene transcription, targeted to putative gene sequences, followed by assay for one or more selected phenotypes.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. patent application Ser. No. 09/395,448, filed Sep. 14, 1999, the disclosure of which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (53):

[0083] A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or functional fragments of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g.,

transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (118):

[0148] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

PGPUB-DOCUMENT-NUMBER: 20020090627

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20020090627 A1

TITLE: 27419, a novel human arginine-N-methyl transferase and uses thereof

PUBLICATION-DATE: July 11, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
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APPL-NO: 09/ 970638

DATE FILED: October 3, 2001

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60237717 20001005 US

US-CL-CURRENT: 435/6, 435/193 , 435/320.1 , 435/325 , 435/69.1 , 514/44 , 514/7 , 536/23.2

ABSTRACT:

The invention provides isolated nucleic acids molecules, designated 27419 nucleic acid molecules, which encode novel methyltransferase family members, preferably **arginine methyltransferase** family members. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing 27419 nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 27419 gene has been introduced or disrupted. The invention still further provides isolated 27419 proteins, fusion proteins, antigenic peptides and anti-27419 antibodies. Diagnostic methods utilizing compositions of the invention are also provided.

[0001] This application claims benefit of priority from U.S. application Ser. No. 60/237,717 filed Oct. 5, 2000, which is hereby incorporated by reference in its entirety.

---------- KWIC ---------

Abstract Paragraph - ABTX (1):

The invention provides isolated nucleic acids molecules, designated 27419 nucleic acid molecules, which encode novel methyltransferase family members, preferably **arginine methyltransferase** family members. The invention also

provides antisense nucleic acid molecules, recombinant expression vectors containing 27419 nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 27419 gene has been introduced or disrupted. The invention still further provides isolated 27419 proteins, fusion proteins, antigenic peptides and anti-27419 antibodies. Diagnostic methods utilizing compositions of the invention are also provided.

Summary of Invention Paragraph - BSTX (4):

[0004] The predominant protein **arginine methyltransferase** is PRMT1, which contributes over 90% of known **arginine methyltransferase** activity within cells. The enzyme is found in mammalian cells as a large molecular weight complex ranging from 300-400 kDa. Because the **arginine methyltransferase** reaction is highly specific with respect to both the configuration of the amino acid residue and the site of the addition, it is expected that unique domain structures for substrate recognition and peptide-methyl binding are located within the enzyme molecule. **Arginine methyltransferase** catalyzes the formation of asymmetric omega-NG, NG-dimethylarginine residues by transferring methyl groups from S-adenosyl-L-methionine to guanidino groups of arginine residues (Tang (2000) J Biol Chem 275(11):7723-30).

Summary of Invention Paragraph - BSTX (11):

[0010] In another aspect, the invention features, 27419 polypeptides, and biologically active or antigenic fragments thereof that are useful, e.g., as reagents or targets in assays applicable to treatment and diagnosis of 27419-mediated or -related disorders. In another embodiment, the invention provides 27419 polypeptides having a 27419 activity. Preferred polypeptides are 27419 proteins including at least one **arginine methyltransferase** family domain, and, preferably, having a 27419 activity, e.g., a 27419 activity as described herein.

Detail Description Paragraph - DETX (15):

[0042] The 27419 protein contains a significant number of structural characteristics in common with members of the **arginine methyltransferase** family. The term "family" when referring to the protein and nucleic acid molecules of the invention means two or more proteins or nucleic acid molecules having a common structural domain or motif and having sufficient amino acid or nucleotide sequence homology as defined herein. Such family members can be naturally or non-naturally occurring and can be from either the same or different species. For example, a family can contain a first protein of human origin as well as other distinct proteins of human origin, or alternatively, can contain homologues of non-human origin, e.g., rat or mouse proteins. Members of a family can also have common functional characteristics.

Detail Description Paragraph - DETX (16):

[0043] As used herein, the term "**arginine methyltransferase** family" includes a molecule which is involved in the signal transduction pathway associated with a large number of extracellular signals. The **arginine methyltransferase** family can interact with a large number of molecules following activation by

interaction with GTP. **Arginine methyltransferase** family molecules are involved in the growth, development, and proliferation of cells, in the regulation of cellular homeostasis, in the metabolism and catabolism of biochemical molecules necessary for energy production or storage, in intra- or intercellular signaling, and in metabolism or catabolism of metabolically important biomolecules. The **arginine methyltransferase** family molecules of the present invention provide novel diagnostic targets and therapeutic agents to control **arginine methyltransferase** family-associated disorders.

Detail Description Paragraph - DETX (17):

[0044] As used herein, a "27419 activity", "biological activity of 27419" or "functional activity of 27419", refers to an activity exerted by a 27419 protein, polypeptide or nucleic acid molecule on e.g., a 27419-responsive cell or on a 27419 substrate, e.g., a lipid or protein substrate, as determined in vivo or in vitro. In one embodiment, a 27419 activity is a direct activity, such as an association with a 27419 target molecule. A "target molecule" or "binding partner" is a molecule with which a 27419 protein binds or interacts in nature, e.g., a molecule in which the 27419 protein activates an **arginine methyltransferase** activity. A 27419 activity can also be an indirect activity, e.g., a cellular signaling activity mediated by interaction of the 27419 protein with a 27419 ligand. For example, the 27419 proteins of the present invention can have one or more of the following activities: 1) cell transversal through the cell cycle, 2) cell differentiation, 3) cell migration and patterning, 4) programmed cell death, 5) modulation of signal transduction, mediation of cell proliferation, 6) regulation of cellular protein trafficking and 7) the ability to antagonize or inhibit, competitively or non-competitively, any of 1-6. Thus, the 27419 molecules can act as novel diagnostic targets and therapeutic agents for controlling **arginine methyltransferase**-related disorders, for example, such as those diseases associated with the activities described above. As the 27419 molecules have homology to known **arginine methyltransferases**, they are expected to be involved in controlling similar disorders.

Detail Description Paragraph - DETX (18):

[0045] To identify the presence of a "**arginine methyltransferase** family" domain in a 27419 protein sequence, and make the determination that a polypeptide or protein of interest has a particular profile, the amino acid sequence of the protein can be searched against a database of HMMs (e.g., the Pfam database, release 2.1) using the default parameters (http://www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for MILPAT0063 and a score of 15 is the default threshold score for determining a hit. Alternatively, the threshold score for determining a hit can be lowered (e.g., to 8 bits). A description of the Pfam database can be found in Sonhammer et al., (1997) Proteins 28(3):405-420 and a detailed description of HMMs can be found, for example, in Gribskov et al., (1990) Meth. Enzymol. 183:146-159; Gribskov et al., (1987) Proc. Natl. Acad. Sci. USA 84:4355-4358; Krogh et al., (1994) J. Mol. Biol. 235:1501-1531; and Stultz et al., (1993) Protein Sci. 2:305-314, the contents of which are incorporated herein by reference.

Detail Description Paragraph - DETX (38):

[0065] As used herein, an "**arginine methyltransferase** family-associated disorder" includes a disorder, disease or condition which is caused or characterized by a misregulation (e.g., downregulation or upregulation) of an **arginine methyltransferase** family-mediated activity. **Arginine methyltransferase** family-associated disorders can detrimentally affect cellular functions such as cellular proliferation, growth, differentiation, or migration, cellular regulation of homeostasis, inter- or intra-cellular communication; tissue function, such as cardiac function or musculoskeletal function; systemic responses in an organism, such as nervous system responses, hormonal responses (e.g., insulin response), or immune responses; and protection of cells from toxic compounds (e.g., carcinogens, toxins, mutagens, and toxic byproducts of metabolic activity (e.g., reactive oxygen species)). Accordingly, 27419 protein may mediate various disorders, including cellular proliferative and/or differentiative disorders, hormonal disorders, immune disorders, brain disorders, heart disorders, and pain and metabolic disorders. As the 27419 polypeptides of the invention may modulate 27419-mediated activities, they may be useful for developing novel diagnostic and therapeutic agents for 27419-mediated or related disorders, as described below.

Detail Description Paragraph - DETX (39):

[0066] **Arginine methyltransferase**-family proteins are essential for cellular signal transduction response following DNA damage. **Arginine methyltransferase**-family proteins have been shown to posttranslationally modify proteins following induction from TIS21 gene expression, a gene activated in response to DNA damage through a p53-dependent pathway. The activity of the **arginine methyltransferase** in response to DNA damage plays a role in the delay of the cell cycle and triggering of apoptosis. Thus the family of **arginine methyltransferases** is involved in cellular integrity associated with the p53 tumour suppressor, and may be a component in prevention of various cancers. The 27419 polypeptides share a common domain with known **arginine methyltransferase**-family members and is expected to have similar effects in cell proliferation. Accordingly, 27419 may play a role in cell proliferation and cancer, inflammation and apoptosis, and thus the 27419 compositions of the invention (e.g., nucleic acids, polypeptides, proteins, antibodies) can be used to modulate cell proliferation, e.g., in cancer, inflammation or apoptosis, and furthermore can be used in screening assays to identify agents for modulating cell proliferation, as well as in detection or diagnostic assays to identify conditions involving aberrant cell proliferation.

Detail Description Paragraph - DETX (46):

[0073] **Arginine methyltransferase** family-associated or related disorders also include hormonal disorders, such as conditions or diseases in which the production and/or regulation of hormones in an organism is aberrant. Examples of such disorders and diseases include type I and type II diabetes mellitus, pituitary disorders (e.g., growth disorders), thyroid disorders (e.g., hypothyroidism or hyperthyroidism), and reproductive or fertility disorders (e.g., disorders which affect the organs of the reproductive system, e.g., the

prostate gland, the uterus, or the vagina; disorders which involve an imbalance in the levels of a reproductive hormone in a subject; disorders affecting the ability of a subject to reproduce; and disorders affecting secondary sex characteristic development, e.g., adrenal hyperplasia).

Detail Description Paragraph - DETX (47):

[0074] **Arginine methyltransferase** family-associated or related disorders also include immune disorders, such as autoimmune disorders or immune deficiency disorders, e.g., congenital X-linked infantile hypogammaglobulinemia, transient hypogammaglobulinemia, common variable immunodeficiency, selective IgA deficiency, chronic mucocutaneous candidiasis, or severe combined immunodeficiency.

Detail Description Paragraph - DETX (58):

[0085] A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of 27419 (e.g., the sequence of SEQ ID NO:1, SEQ ID NO:3, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____) without abolishing or more preferably, without substantially altering a biological activity, whereas an "essential" amino acid residue results in such a change. For example, amino acid residues that are conserved among the polypeptides of the present invention, e.g., those present in the **arginine methyltransferase** family domain, are predicted to be particularly unamenable to alteration.

Detail Description Paragraph - DETX (60):

[0087] As used herein, a "biologically active portion" of a 27419 protein includes a fragment of a 27419 protein which participates in an interaction between a 27419 molecule and a non-27419 molecule. Biologically active portions of a 27419 protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the 27419 protein, e.g., the amino acid sequence shown in SEQ ID NO:2, which include less amino acids than the full length 27419 proteins, and exhibit at least one activity of a 27419 protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the 27419 protein, e.g., **arginine methyltransferase** family activity. A biologically active portion of a 27419 protein can be a polypeptide which is, for example, 10, 25, 50, 100, 200 or more amino acids in length. Biologically active portions of a 27419 protein can be used as targets for developing agents which modulate a 27419 mediated activity, e.g., **arginine methyltransferase** family activity.

Detail Description Paragraph - DETX (78):

[0105] A nucleic acid molecule of the invention can include only a portion of the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:3, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____. For example, such a nucleic acid molecule can include a fragment which can be used as a probe or primer or a fragment encoding a portion of a 27419 protein, e.g., an immunogenic or biologically active portion of a 27419 protein. A fragment can comprise: nucleotides 589-1137 of SEQ ID NO:1, which encodes an **arginine methyltransferase** family domain of human 27419.

The nucleotide sequence determined from the cloning of the 27419 gene allows for the generation of probes and primers designed for use in identifying and/or cloning other 27419 family members, or fragments thereof, as well as 27419 homologues, or fragments thereof, from other species.

Detail Description Paragraph - DETX (80):

[0107] A nucleic acid fragment can include a sequence corresponding to a domain, region, or functional site described herein. A nucleic acid fragment can also include one or more domain, region, or functional site described herein. Thus, for example, the nucleic acid fragment can include an **arginine methyltransferase** family domain. In a preferred embodiment the fragment is at least, 50, 100, 200, 300, 400, 500, 600, 700, or 900 base pairs in length.

Detail Description Paragraph - DETX (83):

[0110] A probe or primer can be derived from the sense or anti-sense strand of a nucleic acid which encodes an **arginine methyltransferase** family domain (e.g., about nucleotides 589-1137 of SEQ ID NO:1).

Detail Description Paragraph - DETX (84):

[0111] In another embodiment a set of primers is provided, e.g., primers suitable for use in a PCR, which can be used to amplify a selected region of a 27419 sequence, e.g., a region described herein. The primers should be at least 5, 10, or 50 base pairs in length and less than 100, or less than 200, base pairs in length. The primers should be identical, or differs by one base from a sequence disclosed herein or from a naturally occurring variant. E.g., primers suitable for amplifying all or a portion of any of the following regions are provided: an **arginine methyltransferase** family domain (e.g., about nucleotides 589-1137 of SEQ ID NO:1).

Detail Description Paragraph - DETX (86):

[0113] A nucleic acid fragment encoding a "biologically active portion of a 27419 polypeptide" can be prepared by isolating a portion of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or the nucleotide sequence of the DNA insert of the plasmid deposited with ATCC as Accession Number _____, which encodes a polypeptide having a 27419 biological activity (e.g., the biological activities of the 27419 proteins as described herein), expressing the encoded portion of the 27419 protein (e.g., by recombinant expression in vitro) and assessing the activity of the encoded portion of the 27419 protein. For example, a nucleic acid fragment encoding a biologically active portion of 27419 includes an **arginine methyltransferase** family domain (e.g., about nucleotides 589-1137 of SEQ ID NO:1). A nucleic acid fragment encoding a biologically active portion of a 27419 polypeptide, may comprise a nucleotide sequence which is greater than 300-1200 or more nucleotides in length.

Detail Description Paragraph - DETX (93):

[0120] Orthologs, homologs, and allelic variants can be identified using methods known in the art. These variants comprise a nucleotide sequence encoding a polypeptide that is 50%, at least about 55%, typically at least

about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more identical to the amino acid sequence shown in SEQ ID NO:2 or a fragment of this sequence. Such nucleic acid molecules can readily be obtained as being able to hybridize under stringent conditions, to the nucleotide sequence shown in SEQ ID NO:3 or a fragment of this sequence. Nucleic acid molecules corresponding to orthologs, homologs, and allelic variants of the 27419 cDNAs of the invention can further be isolated by mapping to the same chromosome or locus as the 27419 gene. Preferred variants include those that are correlated with **arginine methyltransferase** family activity.

Detail Description Paragraph - DETX (94):

[0121] Allelic variants of 27419, e.g., human 27419, include both functional and non-functional proteins. Functional allelic variants are naturally occurring amino acid sequence variants of the 27419 protein within a population that maintain the ability to have **arginine methyltransferase** activity. Functional allelic variants will typically contain only conservative substitution of one or more amino acids of SEQ ID NO:2, or substitution, deletion or insertion of non-critical residues in non-critical regions of the protein. Non-functional allelic variants are naturally-occurring amino acid sequence variants of the 27419, e.g., human 27419, protein within a population that do not have the ability to activate signal transduction. Non-functional allelic variants will typically contain a non-conservative substitution, a deletion, or insertion, or premature truncation of the amino acid sequence of SEQ ID NO:2, or a substitution, insertion, or deletion in critical residues or critical regions of the protein.

Detail Description Paragraph - DETX (113):

[0140] (i) activation of an **arginine methyltransferase** activity;

Detail Description Paragraph - DETX (116):

[0143] (iv) it has an **arginine methyltransferase** family domain which preferably has an overall sequence similarity of about 70%, 80%, 90% or 95% with amino acid residues 186-368 of SEQ ID NO:2;

Detail Description Paragraph - DETX (118):

[0145] In a preferred embodiment the 27419 protein, or fragment thereof, differs from the corresponding sequence in SEQ ID NO:2. In one embodiment it differs by at least one but by less than 15, 10 or 5 amino acid residues. In another it differs from the corresponding sequence in SEQ ID NO:2 by at least one residue but less than 20%, 15%, 10% or 5% of the residues in it differ from the corresponding sequence in SEQ ID NO:2. (If this comparison requires alignment the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.) The differences are, preferably, differences or changes at a non-essential residue or a conservative substitution. In a preferred embodiment the differences are not in the **arginine methyltransferase** family domain. In another preferred embodiment one or more differences are in non-active site residues, e.g. outside of the **arginine methyltransferase** family domain.

Detail Description Paragraph - DETX (120):

[0147] In one embodiment, a biologically active portion of a 27419 protein includes an **arginine methyltransferase** family domain. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native 27419 protein.

Detail Description Paragraph - DETX (135):

[0162] Cell based assays can be exploited to analyze a variegated 27419 library. For example, a library of expression vectors can be transfected into a cell line, e.g., a cell line, which ordinarily responds to 27419 in a substrate-dependent manner. The transfected cells are then contacted with 27419 and the effect of the expression of the mutant on signaling by the 27419 substrate can be detected, e.g., by measuring **arginine methyltransferase** family activity. Plasmid DNA can then be recovered from the cells which score for inhibition, or alternatively, potentiation of signaling by the 27419 substrate, and the individual clones further characterized.

Detail Description Paragraph - DETX (142):

[0169] Fragments of 27419 which include, e.g., residues 1-40 of SEQ ID NO:2 can be, e.g., used as immunogens, or used to be hydrophilic regions of the 27419 protein. Similarly, a fragment of 27419 which includes, e.g., residues 185-195 of SEQ ID NO:2 can be used to make an antibody against what is believed to be a hydrophobic region of the 27419 protein; a fragment of 27419 which includes, e.g., residues 186-368 of SEQ ID NO:2 can be used to make an antibody against what is believed to be the **arginine methyltransferase** family region of the 27419 protein.

Detail Description Paragraph - DETX (182):

[0209] The isolated nucleic acid molecules of the invention can be used, for example, to express a 27419 protein (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect a 27419 mRNA (e.g., in a biological sample) or a genetic alteration in a 27419 gene, and to modulate 27419 activity, as described further below. The 27419 proteins can be used to treat disorders characterized by insufficient or excessive production of a 27419 substrate or production of 27419 inhibitors. In addition, the 27419 proteins can be used to screen for naturally occurring 27419 substrates, to screen for drugs or compounds which modulate 27419 activity, as well as to treat disorders characterized by insufficient or excessive production of 27419 protein or production of 27419 protein forms which have decreased, aberrant or unwanted activity compared to 27419 wild-type protein. Such disorders include those characterized by aberrant signaling or aberrant, e.g., **arginine methyltransferase** activity. Moreover, the anti-27419 antibodies of the invention can be used to detect and isolate 27419 proteins, regulate the bioavailability of 27419 proteins, and modulate 27419 activity.

Detail Description Paragraph - DETX (190):

[0217] In one embodiment, an assay is a cell-based assay in which a cell which expresses a 27419 protein or biologically active portion thereof is contacted with a test compound, and the ability of the test compound to modulate 27419 activity is determined. Determining the ability of the test compound to modulate 27419 activity can be accomplished by monitoring, for example, **arginine methyltransferase** family activity. The cell, for example, can be of mammalian origin, e.g., human. Cell homogenates, or fractions, preferably membrane containing fractions, can also be tested.

Detail Description Paragraph - DETX (196):
[0223] In one embodiment, assays are performed where the ability of an agent to block **arginine methyltransferase** family activity within a cell is evaluated.

Detail Description Paragraph - DETX (237):
[0264] The 27419 nucleotide sequences described herein can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes which can be used in, for example, an in situ hybridization technique, to identify a specific tissue, e.g., a tissue containing **arginine methyltransferase** family activity. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such 27419 probes can be used to identify tissue by species and/or by organ type.

Detail Description Paragraph - DETX (242):
[0269] Such disorders include, e.g., a disorder associated with the misexpression of 27419, or **arginine methyltransferase** related disorder.

Detail Description Paragraph - DETX (270):
[0297] The prognostic assays described herein can be used to determine whether a subject can be administered an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant or unwanted 27419 expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a cellular **arginine methyltransferase** related disorder.

Detail Description Paragraph - DETX (271):
[0298] The methods of the invention can also be used to detect genetic alterations in a 27419 gene, thereby determining if a subject with the altered gene is at risk for a disorder characterized by misregulation in 27419 protein activity or nucleic acid expression, such as a cellular **arginine methyltransferase** related disorder. In preferred embodiments, the methods include detecting, in a sample from the subject, the presence or absence of a genetic alteration characterized by at least one of an alteration affecting the integrity of a gene encoding a 27419-protein, or the mis-expression of the 27419 gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of 1) a deletion of one or more nucleotides from a 27419 gene; 2) an addition of one or more nucleotides to a 27419 gene; 3) a substitution of one or more nucleotides of a 27419 gene, 4) a

chromosomal rearrangement of a 27419 gene; 5) an alteration in the level of a messenger RNA transcript of a 27419 gene, 6) aberrant modification of a 27419 gene, such as of the methylation pattern of the genomic DNA, 7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a 27419 gene, 8) a non-wild type level of a 27419-protein, 9) allelic loss of a 27419 gene, and 10) inappropriate post-translational modification of a 27419-protein.

Detail Description Paragraph - DETX (350):

[0377] The 27419 molecules of the present invention, as well as agents, or modulators which have a stimulatory or inhibitory effect on 27419 activity (e.g., 27419 gene expression) as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) 27419 associated disorders (e.g., cellular **arginine methyltransferase** related disorders) associated with aberrant or unwanted 27419 activity. In conjunction with such treatment, pharmacogenomics (i.e., the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, a physician or clinician may consider applying knowledge obtained in relevant pharmacogenomics studies in determining whether to administer a 27419 molecule or 27419 modulator as well as tailoring the dosage and/or therapeutic regimen of treatment with a 27419 molecule or 27419 modulator.

Detail Description Paragraph - DETX (362):

[0389] The plurality of capture probes can be a plurality of nucleic acid probes each of which specifically hybridizes, with an allele of 27419. Such methods can be used to diagnose a subject, e.g., to evaluate risk for a disease or disorder, to evaluate suitability of a selected treatment for a subject, to evaluate whether a subject has a disease or disorder. 27419 is associated with **arginine methyltransferase** family activity, thus it is useful for disorders associated with abnormal lipid metabolism.

Detail Description Paragraph - DETX (374):

[0401] The present invention therefore provides a medium for holding instructions for performing a method for determining whether a subject has a **arginine methyltransferase**-associated or another 27419-associated disease or disorder or a pre-disposition to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, wherein the method comprises the steps of determining 27419 sequence information associated with the subject and based on the 27419 sequence information, determining whether the subject has a **arginine methyltransferase**-associated or another 27419-associated disease or disorder and/or recommending a particular treatment for the disease, disorder, or pre-disease condition.

Detail Description Paragraph - DETX (375):

[0402] The present invention further provides in an electronic system and/or in a network, a method for determining whether a subject has a **arginine**

methyltransferase-associated or another 27419-associated disease or disorder or a pre-disposition to a disease associated with 27419, wherein the method comprises the steps of determining 27419 sequence information associated with the subject, and based on the 27419 sequence information, determining whether the subject has a **arginine methyltransferase**-associated or another 27419-associated disease or disorder or a pre-disposition to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, and/or recommending a particular treatment for the disease, disorder, or pre-disease condition. The method may further comprise the step of receiving phenotypic information associated with the subject and/or acquiring from a network phenotypic information associated with the subject.

Detail Description Paragraph - DETX (376):

[0403] The present invention also provides in a network, a method for determining whether a subject has a **arginine methyltransferase**-associated or another 27419-associated disease or disorder or a pre-disposition to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, said method comprising the steps of receiving 27419 sequence information from the subject and/or information related thereto, receiving phenotypic information associated with the subject, acquiring information from the network corresponding to 27419 and/or corresponding to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, and based on one or more of the phenotypic information, the 27419 information (e.g., sequence information and/or information related thereto), and the acquired information, determining whether the subject has a **arginine methyltransferase**-associated or another 27419-associated disease or disorder or a pre-disposition to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder. The method may further comprise the step of recommending a particular treatment for the disease, disorder, or pre-disease condition.

Detail Description Paragraph - DETX (377):

[0404] The present invention also provides a business method for determining whether a subject has a **arginine methyltransferase**-associated or another 27419-associated disease or disorder or a pre-disposition to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, said method comprising the steps of receiving information related to 27419 (e.g., sequence information and/or information related thereto), receiving phenotypic information associated with the subject, acquiring information from the network related to 27419 and/or related to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, and based on one or more of the phenotypic information, the 27419 information, and the acquired information, determining whether the subject has a **arginine methyltransferase**-associat- ed or another 27419-associated disease or disorder or a pre-disposition to a **arginine methyltransferase**-associated or another 27419-associated disease or disorder. The method may further comprise the step of recommending a particular treatment for the disease, disorder, or pre-disease condition.

Detail Description Paragraph - DETX (380):

[0407] In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development of a **arginine methyltransferase**-associated or another 27419-associated disease or disorder, progression of **arginine methyltransferase**-associated or another 27419-associated disease or disorder, and processes, such a cellular transformation associated with the **arginine methyltransferase**-associated or another 27419-associated disease or disorder.

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DOCUMENT-IDENTIFIER: US 20020081614 A1

TITLE: Functional genomics using zinc finger proteins

PUBLICATION-DATE: June 27, 2002

INVENTOR-INFORMATION:

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APPL-NO: 09/ 925796

DATE FILED: August 9, 2001

RELATED-US-APPL-DATA:

child 09925796 A1 20010809

parent continuation-of 09395448 19990914 US PENDING

US-CL-CURRENT: 435/6, 435/7.21 , 702/19

ABSTRACT:

0 The present invention provides methods of regulating gene expression using recombinant zinc finger proteins, for functional genomics and target validation applications.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is related to U.S. Ser. No. 09/229,007, filed Jan. 12, 1999, and U.S. Ser. No. 09/229,037, filed Jan. 12, 1999, herein both incorporated by reference in their entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (37):

[0072] A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors

include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detail Description Paragraph - DETX (98):

[0133] Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

US-PAT-NO: 6599692

DOCUMENT-IDENTIFIER: US 6599692 B1

TITLE: Functional genomics using zinc finger proteins

DATE-ISSUED: July 29, 2003

INVENTOR-INFORMATION:

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APPL-NO: 09/ 395448

DATE FILED: September 14, 1999

PARENT-CASE:

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to U.S. application Ser. No. 09/229,007, filed Jan. 12, 1999, and U.S. application Ser. No. 09/229,037, filed Jan. 12, 1999, are both incorporated by reference in their entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

Not applicable.

US-CL-CURRENT: 435/4, 435/6 , 536/23.1

ABSTRACT:

The present invention provides methods of regulating gene expression using recombinant zinc finger proteins, for functional genomics and target validation applications.

55 Claims, 5 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 5

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Detailed Description Text - DETX (37):

A "**transcriptional activator" and a "transcripti nal** repressor" refer to proteins or effector domains of proteins that have the ability to modulate

transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP 16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detailed Description Text - DETX (86):

Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

US-PAT-NO: 6593114

DOCUMENT-IDENTIFIER: US 6593114 B1

TITLE: Staphylococcus aureus polynucleotides and sequences

DATE-ISSUED: July 15, 2003

INVENTOR-INFORMATION:

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APPL-NO: 08/ 956171

DATE FILED: October 20, 1997

PARENT-CASE:

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of and claims priority under 35 U.S.C. .sctn. 120 to U.S. patent application Ser. No. 08/781,986, filed Jan. 3, 1997 (pending), which is a non-provisional of and claims benefit under 35 U.S.C. .sctn. 119(e) of U.S. Provisional Application Ser. No. 60/009,861 filed Jan. 5, 1996.

Reference to a Sequence Listing Provided on Compact Disc

This application refers to a "Sequence Listing", which is provided as an electronic document on two identical compact discs (CD-R), labeled "Copy 1" and "Copy 2." These compact discs each contain the electronic document, filename "PB248P1 sequence listing.txt" (6,143,313 bytes in size, created on Jan. 24, 2002), which is hereby incorporated in its entirety herein.

US-CL-CURRENT: 435/91.41, 435/252.3 , 435/254.11 , 435/257.2 , 435/320.1 , 435/325 , 435/91.4 , 536/23.7

ABSTRACT:

The present invention provides polynucleotide sequences of the genome of Staphylococcus aureus, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which

facilitate its use.

15 Claims, 2 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 2

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Detailed Description Paragraph Table - DETL (24):
[Caenorhabditis elegans] 706 2 355 149 gi.vertline.804808 unknown protein [Rattus norvegicus] 66 46 207 734 2 512 351 gi.vertline.1519085 phosphatidylcholine binding immunoglobulin heavy chain IgM 66 60 162 variable region [Mus musculus] 740 1 3 317 gi.vertline.1209272 argininosuccinate lyase [Campylobacter jejuni] 66 42 315 764 1 310 747 gi.vertline.435296 alkaline phosphatase like protein [Lactococcus lactis] 66 42 438 pir.vertline.S39339.vertline.S39339 alkaline phosphatase-like protein - Lactococcus actis 852 1 171 4 gi.vertline.536955 CG Site No. 361 [Escherichia coli] 66 43 168 886 1 3 158 gi.vertline.289272 ferrichrome-binding protein [Bacillus subtilis] 66 44 156 889 1 232 2 gi.vertline.833061 HCMVUL77 (AA 1-642) [Human cytomegalovirus] 66 66 231 893 1 2 247 gi.vertline.149008 putative [Helicobacter pylori] 66 45 246 900 1 733 41 gi.vertline.580842 F3 [Bacillus subtilis] 66 51 693 906 2 1473 646 gi.vertline.790945 aryl-alcohol dehydrogenase [Bacillus subtilis] 66 53 828 947 1 79 549 gi.vertline.410117 diaminopimelate decarboxylase [Bacillus subtilis] 66 47 471 950 1 552 4 gi.vertline.48713 orf145 [Staphylococcus aureus] 66 35 549 955 2 89 475 gi.vertline.1204390 uridine kinase (uridine monophosphokinase) [Haemophilus 66 50 387 influenzae] 981 2 997 686 gi.vertline.457146 rhoptry protein [Plasmodium yoelii] 66 38 312 986 1 25 315 gi.vertline.305002 ORF_f356 [Escherichia coli] 66 31 291 1057 1 3 203 gi.vertline.1303853 YqgF [Bacillus subtilis] 66 40 201 1087 1 1 294 gi.vertline.575913 unknown [Saccharomyces cerevisiae] 66 53 294 1105 1 1 231 gi.vertline.1045799 methylgalactoside permease ATP-binding protein [Mycoplasma 66 46 231 genitalium] 1128 1 2 574 gi.vertline.1001493 hypothetical protein [Synechocystis sp.] 66 46 573 1150 1 250 2 gi.vertline.1499034 M. jannaschii predicted coding region MJ0255 [Methanococcus 66 40 249 jannaschii] 1180 2 453 199 gi.vertline.215908 DNA polymerase (g43) [Bacteriophage T4] 66 46 255 1208 1 587 51 gi.vertline.1256653 DNA-binding protein [Bacillus subtilis] 66 58 537 1342 1 1 402 gi.vertline.1208474 hypothetical protein [Synechocystis sp.] 66 53 402 1761 2 398 207 gi.vertline.215811 tail fiber protein [Bacteriophage T3] 66 50 192 1983 1 251 3 gi.vertline.1045935 DNA helicase II [Mycoplasma genitalium] 66 40 249 2103 2 176 400 gi.vertline.929798 precursor for the major merozoite surface antigens [Plasmodium 66 46 225 alciparum] 2341 1 188 3 gi.vertline.1256623 exodeoxyribonuclease [Bacillus subtilis] 66 38 186 2458 1 164 3 gi.vertline.1019410 unknown [Schizosaccharomyces pombe] 66 47 162 2505 1 235 2 gi.vertline.1510394 putative transcriptional regulator [Methanococcus jannaschii] 66 39 234 2525 1 280 2 gi.vertline.1000695 cytotoxin L [Clostridium sordellii] 66 44 279 2935 1 3 275 gi.vertline.765073 autolysin [Staphylococcus aureus] 66 47 273 3005 1 114 305 gi.vertline.1205784 heterocyst maturation protein [Haemophilus influenzae] 66

46 192 3048 1 80 277 gi.vertline.1303813 YqeW [Bacillus subtilis] 66 42 198 3071 1 1 189 gi.vertline.1070014 protein-dependent [Bacillus subtilis] 66 41 189 3081 1 225 46 gi.vertline.984212 unknown [Schizosaccharomyces pombe] 66 44 180 3090 2 386 192 gi.vertline.1204987 DNA polymerase III, alpha chain [Haemophilus influenzae] 66 48 195 3318 1 1 387 gi.vertline.1009366 Respiratory nitrate reductase [Bacillus subtilis] 66 49 387 3739 1 400 2 gi.vertline.1109684 ProV [Bacillus subtilis] 66 47 399 3796 1 202 2 gi.vertline.853760 acyl-CoA dehydrogenase [Bacillus subtilis] 66 60 201 3924 1 347 99 gi.vertline.563952 gluconate permease [Bacillus licheniformis] 66 46 249 4240 1 3 350 gi.vertline.151259 HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] 66 51 348 pir.vertline.A44756.vertline.A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp. 4604 1 7 234 pir.vertline.A26713.vertline.BHHC hemocyanin subunit II - Atlantic horseshoe crab 66 46 228 4 9 8845 9750 gi.vertline.145646 cynR [Escherichia coli] 65 35 906 6 5 2708 3565 gi.vertline.887824 ORF_o310 [Escherichia coli] 65 47 858 13 1 998 3 gi.vertline.143402 recombination protein (ttg start codon) [Bacillus subtilis] gi.vertline.1303923 65 44 996 RecN [Bacillus subtilis] 15 7 2493 3524 gi.vertline.1403126 czcD gene product [Alcaligenes eutrophus] 65 38 1032 18 3 1372 836 gi.vertline.349187 acyltransferase [Saccharomyces cerevisiae] 65 50 537 21 3 1467 2492 gi.vertline.149518 phosphoribosyl anthranilate transferase [Lactococcus lactis] 65 52 1026 pir.vertline.S35126.vertline.S35126 anthranilate phosphoribosyltransferase (EC .4.2.18) - Lactococcus lactis subsp. lactis 25 4 3374 4312 gi.vertline.1502420 malonyl-CoA:Acyl carrier protein transacylase [Bacillus subtilis] 65 44 939 27 2 390 626 gi.vertline.1212729 YqhJ [Bacillus subtilis] 65 45 237 31 12 10387 9734 gi.vertline.509245 D-hydroxyisocaproate dehydrogenase [Lactobacillus delbrueckii] 65 41 654 38 24 19172 19528 gi.vertline.547519 H-protein [Flaveria cronquistii] 65 41 357 44 2 790 1746 gi.vertline.405882 yeiK [Escherichia coli] 65 46 957 44 12 8832 8308 gi.vertline.1205905 molybdenum cofactor biosynthesis protein [Haemophilus influenzae] 65 50 525 45 8 6635 7588 gi.vertline.493074 ApbA protein [Salmonella typhimurium] 65 46 954 51 2 580 1503 gi.vertline.580897 OppB gene product [Bacillus subtilis] 65 45 924 52 1 225 953 gi.vertline.1205518 NAD(P)H-flavin oxidoreductase [Haemophilus influenzae] 65 45 729 55 4 1058 777 pir.vertline.A44459.vertline.A444 troponin T beta TnT-5 - rabbit 65 41 282 67 9 7421 8272 gi.vertline.143607 sporulation protein [Bacillus subtilis] 65 42 852 73 5 4446 5375 gi.vertline.1204896 lysophospholipase L2 [Haemophilus influenzae] 65 37 930 74 1 478 2 gi.vertline.1204844 H. influenzae predicted coding region HI0594 [Haemophilus 65 50 477 influenzae] 77 1 2 757 gi.vertline.1046082 M. genitalium predicted coding region MG372 [Mycoplasma 65 46 756 genitalium] 77 2 795 1433 gi.vertline.1222116 permease [Haemophilus influenzae] 65 37 639 81 3 3454 2180 gi.vertline.1001708 hypothetical protein [Synechocystis sp.] 65 49 1275 91 7 8357 8166 gi.vertline.1399263 cystathionine beta-lyase [Emericella nidulans] 65 40 192 98 3 1608 1988 gi.vertline.467423 unknown [Bacillus subtilis] 65 38 381 98 4 2250 2987 gi.vertline.467424 unknown [Bacillus subtilis] 65 45 738 102 3 2119 1640 gi.vertline.1511532 N-terminal acetyltransferase complex, subunit ARD1 [Methanococcus 65 39 480 jannaschii] 102 4 2862 2077 gi.vertline.1204637 H. influenzae predicted coding region HI0388 [Haemophilus 65 32 786 influenzae] 103 9 9841 8831 gi.vertline.142695 S-adenosyl-L-methionine:uroporphyrinogen III **methyltransferas** 65 47 1011 [Bacillus megaterium] 103 10 10119 9799 gi.vertline.710021 nitrite reductase (nirD) [Bacillus subtilis] 65 51 321 106 2 262 1140 gi.vertline.39881 ORF 311 (AA 1-311) [Bacillus subtilis] 65 44 879

109 5 3909 4268 gi.vertline.1204399 glucosamine-6-phosphate deaminase protein [Haemophilus 65 44 360 influenzae] 109 10 7165 8595 gi.vertline.536955 CG Site No. 361 [Escherichia coli] 65 41 1431 110 4 3688 3915 gi.vertline.407881 stringent response-like protein [Streptococcus equisimilis] 65 45 228 pir.vertline.S39975.vertline.S39975 stringent response-like protein - Streptococcus quisimilis 110 5 3882 4295 gi.vertline.407880 ORF1 [Streptococcus equisimilis] 65 50 414 110 6 4231 4380 gi.vertline.1139574 Orf2 [Streptomyces griseus] 65 56 150 112 10 8840 8062 gi.vertline.1204571 H. influenzae predicted coding region HI0318 [Haemophilus 65 52 579 influenzae] 112 12 11288 10527 gi.vertline.710496 **transcriptional activator** protein [Bacillus brevis] 65 32 762 125 1 2 202 gi.vertline.1151158 repeat organellar protein [Plasmodium chabaudi] 65 39 201 126 1 3 422 gi.vertline.37589 precursor [Homo sapiens] 65 46 420 127 11 10733 12658 gi.vertline.1064809 homologous to sp:HTRA_ECOLI [Bacillus subtilis] 65 41 1926 143 8 7004 6465 gi.vertline.216513 mutator mutT (AT-GC transversion) [Escherichia coli] 65 56 540 145 5 3587 3838 gi.vertline.1209768 D02_orf569 [Mycoplasma pneumoniae] 65 27 252 150 4 2841 2200 gi.vertline.1146225 putative [Bacillus subtilis] 65 37 642 166 1 1948 38 gi.vertline.148304 beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] 65 50 1911 pir.vertline.A42296.vertline.A42296 lysozyme 2 (EC 3.2.1.--) precursor - Enterococcus irae (ATCC 9790) 188 6 3195 4178 gi.vertline.151943 ORF3; putative [Rhodobacter capsulatus] 65 46 984 189 9 4785 4588 gi.vertline.58812 ORF IV (AA 1-489) [Figwort mosaic virus] 65 40 198 195 6 5272 2636 gi.vertline.145220 alanyl-tRNA synthetase [Escherichia coli] 65 49 2637 195 7 8104 5609 gi.vertline.882711 exonuclease V alpha-subunit [Escherichia coli] 65 38 2496 206 16 16896 18191 gi.vertline.408115 ornithine acetyltransferase [Bacillus subtilis] 65 53 1296 217 4 3215 2586 gi.vertline.1205974 5' guanylate kinase [Haemophilus influenzae] 65 41 630 220 4 3751 2237 gi.vertline.580920 rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] 65 40 1515 pir.vertline.S06048.vertline.S06048 probable rodD protein - Bacillus subtilis sp.vertline.P13484.vertline.TAGE_BACSU PROBABLE POLY(GLYCEROL- PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52)
(TECHOIC ACID BIOSYNTHESIS ROTEIN E). 236 5 2327 3709 gi.vertline.1146200 DNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis] 65 46 1383 237 3 1902 2513 gi.vertline.149379 HisBd [Lactococcus lactis] 65 46 612 241 4 4195 3422 gi.vertline.1205308 ribonuclease HII (EC 31264) (RNASE HII) [Haemophilus influenzae] 65 50 774 252 1 940 602 gi.vertline.1204989 hypothetical protein (BG:U00022_9) [Haemophilus influenzae] 65 40 339 261 5 3794 2808 gi.vertline.145927 fecD [Escherichia coli] 65 43 987 274 1 3 278 gi.vertline.496558 orfX [Bacillus subtilis] 65 42 276 301 2 815 648 gi.vertline.467418 unknown [Bacillus subtilis] 65 45 168 307 4 2864 2142 gi.vertline.1070014 protein-dependent [Bacillus subtilis] 65 40 723 335 2 1399 512 gi.vertline.146913 N-acetylglucosamine transport protein [Escherichia coli] 65 50 888 pir.vertline.B29895.vertline.WQEC2N phosphotransferase system enzyme II

Detailed Description Paragraph Table - DETL (25):
(EC .7.1.69), N-acetylglucosamine-specific - Escherichia coli sp.vertline.P09323.vertline.PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC OMPONENT (EIIA) 338 5 3170 2220 gi.vertline.1277029 biotin synthase [Bacillus subtilis] 65 49 951 343 3 1490 2800 gi.vertline.143264 membrane-associated protein [Bacillus subtilis] 65 48

1311 344 4 2531 2301 gi.vertline.1050540 tRNA-glutamine synthetase [Lupinus luteus] 65 34 231 358 3 3421 3621 gi.vertline.1146220 NAD+ dependent glycerol-3-phosphate dehydrogenase [Bacillus 65 47 201 subtilis] 364 1 238 699 gi.vertline.1340128 ORF1 [Staphylococcus aureus] 65 51 462 379 1 1 576 gi.vertline.143331 alkaline phosphatase regulatory protein [Bacillus subtilis] 65 40 576 pir.vertline.A27650.vertline.A27650 regulatory protein phoR - Bacillus subtilis sp.vertline.P23545.vertline.PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.--). 379 3 3666 4346 gi.vertline.143268 dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) [Bacillus 65 50 681 ubtilis] 428 1 187 483 gi.vertline.1420465 ORF YOR195w [Saccharomyces cerevisiae] 65 45 297 438 2 272 838 gi.vertline.143498 degS protein [Bacillus subtilis] 65 38 567 444 11 9280 10215 gi.vertline.1204756 ribokinase [Haemophilus influenzae] 65 47 936 449 2 1241 1531 gi.vertline.599848 Na/H antiporter homolog [Lactococcus lactis] 65 41 291 478 2 865 278 gi.vertline.1045942 glycyl-tRNA synthetase [Mycoplasma genitalium] 65 39 588 479 1 517 2 gi.vertline.1498192 putative [Pseudomonas aeruginosa] 65 40 516 480 6 4312 5637 gi.vertline.415662 UDP-N-acetylglucosamine 1-carboxyvinyl transferase [Acinetobacter 65 48 1326 alcoaceticus] 484 1 2 430 gi.vertline.146551 transmembrane protein (kdpD) [Escherichia coli] 65 44 429 499 1 54 932 gi.vertline.603456 reductase [Leishmania major] 65 53 879 505 1 459 4 gi.vertline.1518853 OafA [Salmonella typhimurium] 65 39 456 571 2 883 257 gi.vertline.49399 open reading frame upstream glnE [Escherichia coli] 65 44 627 ir.vertline.S37754.vertline.S37754 hypothetical protein XE (glnE 5' region) - cherichia coli 611 2 270 34 gi.vertline.10961 RAP-2 [Plasmodium falciparum] 65 40 237 705 1 283 2 gi.vertline.710020 nitrite reductase (nirB) [Bacillus subtilis] 65 52 282 712 1 1 177 gi.vertline.289272 ferrichrome-binding protein [Bacillus subtilis] 65 37 177 712 2 196 354 gi.vertline.289272 ferrichrome-binding protein [Bacillus subtilis] 65 37 159 743 1 2 631 gi.vertline.310631 ATP binding protein [Streptococcus gordonii] 65 45 630 749 2 393 779 gi.vertline.467374 single strand DNA binding protein [Bacillus subtilis] 65 29 387 762 1 850 2 gi.vertline.160399 multidrug resistance protein [Plasmodium falciparum] 65 48 849 788 1 85 315 gi.vertline.1129096 unknown protein [Bacillus sp.] 65 35 231 850 1 1 408 gi.vertline.1006604 hypothetical protein [Synechocystis sp.] 65 37 408 908 1 1 444 gi.vertline.1199546 2362 [Saccharomyces cerevisiae] 65 46 444 925 1 1 174 gi.vertline.1256653 DNA-binding protein [Bacillus subtilis] 65 54 174 1031 1 26 232 gi.vertline.238657 AppC=cytochrome d oxidase, subunit I homolog [Escherichia coli, 65 47 207 K12, eptide, 514 aa] 1037 1 262 110 gi.vertline.1491813 gamma-glutamyltranspeptidase [Bacillus subtilis] 65 46 153 1053 1 175 2 gi.vertline.642655 unknown [Rhizobium meliloti] 65 34 174 1149 1 752 105 gi.vertline.1162980 ribulose-5-phosphate 3-epimerase [Spinacia oleracea] 65 48 648 1214 1 495 109 gi.vertline.1205959 lactam utilization protein [Haemophilus influenzae] 65 45 387 1276 1 276 76 pir.vertline.S35493.vertline.S354 site-specific DNA-**methyltransferase** StsI (EC 2.1.1.--) - 65 35 201 Streptococcus sanguis 1276 2 577 254 gi.vertline.473794 `ORF` [Escherichia coli] 65 34 324 2057 1 138 4 gi.vertline.633699 TrsH [Yersinia enterocolitica] 65 21 135 2521 1 169 2 gi.vertline.1045789 hypothetical protein (GB:U14003_76) [Mycoplasma genitalium] 65 41 168 2974 1 297 4 gi.vertline.152052 enantiomerase-selective amidase [Rhodococcus sp.] 65 45 294 3031 1 154 2 pir.vertline.JQ1024.vertline.JQ10 hypothetical 30K protein (DmRP140 5' region) - fruit fly [Drosophila 65 45 153 melanogaster] 3069 1 3 278 gi.vertline.144906 product homologous to E. coli thioredoxin reductase: J. Biol. Chem. 65 46 276 1988) 263:9015-9019, and to F52a protein

of alkyl hydroperoxide eductase from S. typhimurium: J. Biol. Chem. (1990) 265:10535- 10540; pen reading frame A [Clostridium pasteurianum] 3146 1 142 2 gi.vertline.49315 ORF1 gene product [Bacillus subtilis] 65 47 141 3170 1 341 3 gi.vertline.1507711 indolepyruvate decarboxylase [Erwinia herbicola] 65 44 339 3546 1 1 303 gi.vertline.450688 hsdM gene of Ecoprrl gene product [Escherichia coli] 65 42 303 pir.vertline.S38437.vertline.S38437 hsdM protein - Escherichia coli pir.vertline.S09629.vertline.S09629 hypothetical protein A - Escherichia coli (SUB 40-520) 3782 1 2 328 gi.vertline.166412 NADH-glutamate synthase [Medicago sativa] 65 42 327 3990 1 189 4 gi.vertline.1009366 Respiratory nitrate reductase [Bacillus subtilis] 65 53 186 4032 1 308 3 gi.vertline.1323127 ORF YGR087c [Saccharomyces cerevisiae] 65 50 306 4278 2 364 2 gi.vertline.1197667 vitellogenin [Anolis pulchellus] 65 42 363 19 4 4259 5518 gi.vertline.145727 deaD [Escherichia coli] 64 45 1260 19 6 6926 6213 gi.vertline.1016232 ycf27 gene product [Cyanophora paradoxa] 64 36 714 20 8 6454 5855 gi.vertline.765073 autolysin [Staphylococcus aureus] 64 47 600 31 13 11537 10368 gi.vertline.414009 ipa-85d gene product [Bacillus subtilis] 64 45 1170 33 4 2388 4364 gi.vertline.1204696 fructose-permease IIBC component [Haemophilus influenzae] 64 47 1977 36 3 1871 3013 gi.vertline.290503 glutamate permease [Escherichia coli] 64 40 1143 37 6 4065 4409 gi.vertline.39815 orf 2 gene product [Bacillus subtilis] 64 46 345 45 9 7852 8760 gi.vertline.1230585 nucleotide sugar epimerase [Vibrio cholerae O139] 64 53 909 53 3 1540 1899 gi.vertline.1303961 YqjJ [Bacillus subtilis] 64 50 360 56 6 3855 2917 gi.vertline.457514 gltC [Bacillus subtilis] 64 45 939 56 24 30002 30247 gi.vertline.470331 similar to zinc fingers [Caenorhabditis elegans] 64 42 246 62 4 2421 2083 gi.vertline.642655 unknown [Rhizobium meliloti] 64 28 339 85 6 6027 4876 gi.vertline.457702 5-aminoimidazole ribonucleotide-carboxilase [Pichia methanolica] 64 46 1152 pir.vertline.S39112.vertline.S39112 phosphoribosylaminoimidazole carboxylase (EC .1.1.21) - yeast [Pichia methanolica] 96 9 9251 10030 gi.vertline.1511513 ABC transporter, probable ATP-binding subunit [Methanococcus 64 42 780 jannaschii] 100 1 1 600 gi.vertline.765073 autolysin [Staphylococcus aureus] 64 44 600 106 5 3868 4854 gi.vertline.466778 lysine specific permease [Escherichia coli] 64 46 987 123 2 554 270 gi.vertline.467484 unknown [Bacillus subtilis] 64 47 285 127 8 7514 7810 gi.vertline.210061 serotype-specific antigen [African horse sickness virus] 64 28 297 pir.vertline.S27891.vertline.S27891 capsid protein VP2 - African horse sickness virus 131 7 6721 6308 gi.vertline.1511160 M. jannaschii predicted coding region MJ1163 [Methanococcus 64 46 414 jannaschii] 142 5 4817 4179 gi.vertline.1173517 riboflavin synthase alpha subunit [Actinobacillus pleuropneumoniae] 64 44 639 143 1 356 3 pir.vertline.A32950.vertline.A329 probable reductase protein - Leishmania major 64 52 354 149 10 3295 3035 gi.vertline.398151 major surface antigen MSG2 [Pneumocystis carinii] 64 44 261 154 4 2307 1480 gi.vertline.984587 DinP [Escherichia coli] 64 50 828 161 5 3855 4880 gi.vertline.903304 ORF72 [Bacillus subtilis] 64 37 1026 165 1 33 791 gi.vertline.467483 unknown [Bacillus subtilis] 64 38 759 175 6 4844 3333 gi.vertline.1072398 phaD gene product [Rhizobium meliloti] 64 42 1512 188 3 2042 2500 gi.vertline.1001961 MHC class II analog [Staphylococcus aureus] 64 45 459 195 14 13446 13225 gi.vertline.396380 No definition line found [Escherichia coli] 64 47 222 206 15 16429 16938 gi.vertline.304134 argC [Bacillus stearothermophilus] 64 49 510 215 1 282 4 gi.vertline.142359 ORF 6 [Azotobacter vinelandii] 64 39 279 243 7 6928 6038 gi.vertline.414014 ipa-90d gene product [Bacillus subtilis] 64 49 891 258 2 845 360 gi.vertline.664754 P17 [Listeria monocytogenes] 64 38 486

259 1 232 2 gi.vertline.1499663 M. jannaschii predicted coding region MJ0837 [Methanococcus 64 52 231 jannaschii] 263 6 5567 4569 gi.vertline.142828 aspartate semialdehyde dehydrogenase [Bacillus subtilis] 64 48 999 sp.vertline.Q04797.vertline.DHAS_BACSU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE
(EC .2.1.11) (ASA DEHYDROGENASE). 271 1 3 1163 gi.vertline.467091 hflx; B2235_C2_202 [Mycobacterium leprae] 64 44 1161 280 1 173 1450 gi.vertline.1303839 YqfR [Bacillus subtilis] 64 43 1278 293 1 1267 2 gi.vertline.147345 primosomal protein n' [Escherichia coli] 64 45 1266 295 2 742 1488 gi.vertline.459266 Potential membrane spanning protein [Staphylococcus hominis] 64 39 747 pir.vertline.S42932.vertline.S42932 potential membrane spanning protein - taphylococcus hominis 301 5 1446 1267 gi.vertline.580835 lysine decarboxylase [Bacillus subtilis] 64 35 180 315 4 3949 2834 gi.vertline.143396 quinol oxidase [Bacillus subtilis] 64 45 1116 321 1 635 6 gi.vertline.710496 **transcriptional activator** protein [Bacillus brevis] 64 41 630 333 5 4239 3958 gi.vertline.1314295 ORF2; putative 19 kDa protein [Listeria monocytogenes] 64 43 282 342 1 1 549 gi.vertline.142940 ftsA [Bacillus subtilis] 64 38 549 353 3 2324 1770 gi.vertline.537049 ORF_o470 [Escherichia coli] 64 44 555 379 2 827 3658 pir.vertline.S25295.vertline.A328 oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Bacillus 64 47 2832 subtilis 404 6 4429 4839 pir.vertline.A36933.vertline.A369 diacylglycerol kinase homolog - Streptococcus mutans 64 35 411 407 1 1133 246 gi.vertline.969026 OrfX [Bacillus subtilis] 64 41 888 425 1 591 73 gi.vertline.1146177 phosphotransferase system glucose-specific enzyme II [Bacillus 64 44 519 subtilis] 443 6 4082 4798 gi.vertline.147309 purine nucleoside phosphorylase [Escherichia coli] 64 51 717

US-PAT-NO: 6586185

DOCUMENT-IDENTIFIER: US 6586185 B2

TITLE: Use of polypeptides or nucleic acids for the diagnosis or treatment of skin disorders and wound healing and for the identification of pharmacologically active substances

DATE-ISSUED: July 1, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wolf; Eckard	Oberschleissheim	N/A	N/A	DE
Werner; Sabine	Zurich	N/A	N/A	CH
Halle; Jorn-Peter	Penzberg	N/A	N/A	DE
Regenbogen; Johannes	Martinsried	N/A	N/A	DE
Goppelt; Andreas	Munchen	N/A	N/A	DE

APPL-NO: 09/ 886319

DATE FILED: June 20, 2001

PARENT-CASE:

This application claims the benefit of U.S. Provisional Application No. 60/222,081, filed Aug. 1, 2000 and Foreign Application DE 10030149.5 filed Jun. 20, 2000.

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
DE	100 30 149	June 20, 2000

US-CL-CURRENT: 435/6, 424/9.1 , 514/44

ABSTRACT:

Method of using of polypeptides or nucleic acids encoding these for the diagnosis and/or prevention and/or treatment of diseases of skin cells and/or of wound healing and/or its pathological disorders, and their use for the identification of pharmacologically active substance.

3 Claims, 3 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 3

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Brief Summary Text - BSTX (15):

The following polypeptides can be used according to the invention: The tumor susceptibility gene TSG 101 from mouse (SEQ ID No. 1) or human (SEQ ID No. 2) that is known from WO 97/18333 and U.S. Pat. No. 5,892,016 (Li and Cohen, 1996, Cell 85:319-329; Li et al., 1997, Cell 88:143-154). The functional inactivation of TSG 101 in fibroblasts leads to cellular transformation and to the ability to form metastasizing tumors. TSG 101-deficient neo-plastic cells show abnormalities in mitosis associated processes (Xie et al., 1998, Proc. Natl. Acad. Sci. U.S.A. 95:1595-1600). Furthermore, a role as transcriptional modulator is assumed (Sun et al., 1999, Cancer 86:689-696). In addition to the human polypeptide according to SEQ ID No. 2, the splice variant according to SEQ ID No. 82 (SWISSProt: Q99816) can also be used. The tumor suppressor protein MASPIN, that is known from U.S. Pat. No. 5,905,023, U.S. Pat. No. 5,801,001, U.S. Pat. No. 5,470,970 and WO 94/05804 from mouse (SEQ ID No. 3) or human (SEQ ID No. 4) (Zou et al., 1994, Science, 263, 526-529). MASPIN is a serine protease inhibitor (Zhang et al., 1997, Mol. Med. 3:49-59) that is expressed in normal breast and prostate epithelial cells (Zhang et al., 1997, Proc. Natl. Acad. Sci. U.S.A. 94:5673-5678) and plays an essential role in the development of the breast gland (Zhang et al., 1999, Dev. Biol. 215:278-287). The RNA-polymerase I termination factor TTF-I from mouse (SEQ ID No. 5) or human (SEQ ID No. 6) (Evers and Grummt, 1995, Proc. Natl. Acad. Sci. U.S.A. 92:5827-5831). The protein mediates the termination of transcription of ribosomal genes (Kuhn et al., 1990, Nature 344:559-62) as well as the **transcriptional activation** of ribosomal genes in chromatin (Langst et al., 1998, EMBO J. 17:3135-45). The protooncogen B-raf from mouse (SEQ ID No. 7) or human (SEQ ID No. 8), that is known from WO 91/02077 and U.S. Pat. No. 7,745,381 (Miki et al., 1991, Proc. Natl. Acad. Sci. U.S.A. 88:5167-5171; Stephens et al., 1992, Mol. Cell. Biol. 12:3733-3742). The B-raf protooncogene belongs to the Raf-family comprising serine/threonine protein kinases that link the stimulation of growth factor receptors and the activation of mitogen-activated protein kinases (Mason et al., 1999, EMBO J. 18:2137-48). Furthermore, B-Raf can inhibit apoptosis (Erhardt et al., 1999, Mol. Cell. Biol. 19:5308-15). Prothymosin alpha from mouse (SEQ ID No. 9) or human (SEQ ID No. 10), that is known from U.S. Pat. Nos. 4,716,148 and 4,659,694 (Schmidt and Werner, 1991, Biochim. Biophys. Acta. 1088:442-444; Eschenfeldt and Berger, 1986, Proc. Natl. Acad. Sci. U.S.A. 83:9403-9407). It codes for a small acidic nuclear protein that has a role in the proliferation of cells (Tao et al., 1999, J. Cell Physiol. 178:154-63). The GOGLI 4-TRANSMEMBRANE SPANNING TRANSPORTER or MTP (mouse transporter protein) from mouse (SEQ ID No. 11) or human (SEQ ID No. 12) (Hogue et al., 1996, J. Biol. Chem. 271:9801-9808; Nagase et al., 1995, DNA Res. 2:37-43). It is a strongly conserved membrane protein, that is localized in lysosomes and endosomes of mammalian cells. The protein is responsible for the subcellular distribution of a number of different small hydrophobic molecules and contributes to the sensitivity respectively resistance of mammalian cells towards particular active substances (Hogue et al., 1999, J. Biol. Chem. 274:12877-82). For the mouse homologue, an alternative polypeptide truncated at the C terminus by 89 amino acids is formed by an alternative translation initiation site (see SwissProt: Q60961). This murine polypeptide can also be used according to the invention. CCR-1 from mouse (SEQ ID No. 13) or human (SEQ ID No. 14) (Post et al., 1995, J. Immunol. 155:5299-5305) that is an eosinophilic receptor for the CC-chemokin eotaxin (Gao et al., 1996, Biochem. Biophys. Res. Comm. 223:679

-84). CCR-1 is expressed in heart, spleen and lung (Gao and Murphy, 1995, Genomics 29:294-96). The nucleosome binding protein HMG-14 from mouse (SEQ ID No. 15) or human (SEQ ID No. 16) (Landsman and Bustin, 1990, Nucleic Acids Res. 18:5311; Landsman et al., 1986, J. Biol. Chem. 261:16082-16086), that opens up higher order chromatin structures and thus increases the transcription and replication potential of chromatin (Herrera et al., 1999, Mol. Cell. Biol. 19:3466-73). Split hand/foot deleted 1 from mouse (SEQ ID No. 17) or human (SEQ ID No. 18), that is a candidate gene for the autosomal dominant form of "split hand/split foot malformation disorder" that is expressed in limb buds, in the "cranofacial primordia" and in the skin (Crackower et al., 1996, Hum. Mol. Genet. 5:571-9). The orphan receptor TAK1 or TR4 from mouse (SEQ ID No. 19) or human (SEQ ID No. 20) (Hirose et al., 1995, Gene 163:239-242; Hirose et al., 1994, Mol. Endocrinol. 8:1667-1680), that belongs to the superfamily of nuclear hormone receptors (Hirose et al., 1994, Mol, Endocrinol. 8:1667-80). As a homodimer, TR4 influences the multitude of signal transduction pathways, among them retinoic acids, thyroid hormone, vitamin D3 and "ciliary neutrophic factor". Additionally TR4 forms heterodimers with the androgen receptor (Lee et al., 1999, Proc. Natl. Acad. Sci. U.S.A. 96:14724-9). BAF57 from mouse (SEQ ID No. 31) or human (SEQ ID No. 32), that is known from WO 95/14772, which is a part of the chromatin remodeling SWI/SNF complex of higher eukaryotes (Wang et al., 1998, Proc. Natl. Acad. Sci. U.S.A. 95:492-498.) The SWI/SNF complexes regulate the transcription of specific genes by relieving chromatin mediated repression of transcription (Wolffe and Guschin, 2000, J. Struct. Biol. 129:102-122). Additionally, a role has been shown for the switch from expression of fetal to adult globin in mice (Armstrong et al., 1999, Proc. Natl. Acad. Sci. U.S.A. 96:349-54). In addition to the known human and mouse polypeptides, the closely related novel human polypeptide having a significantly different sequence (SEQ ID No. 80) can also be used. The cDNA encoding the polypeptide according to SEQ ID No. 80 is indicated under SEQ ID No. 83. Epidermal growth factor receptor kinase substrate EPS 8 from mouse (SEQ ID No. 33) or human (SEQ ID No. 34), that is known from U.S. Pat. No. 7,935,311, which amplifies the EGF dependent mitogenic signales (Wong et al., 1994, Oncogene 9:3057-3061; Fazioli et al., 1993, EMBO J. 12:3799-3808). Both over-expression as well as constitutive phosphorylation of EPS 8 has been described in connection with tumor development (Matoskova et al., 1995, Mol. Cell Biol. 15:3805-3812). KIAA1247 from human (SEQ ID No. 36), that according to WO 99/34004 can be applied as a marker protein for cancer metastasis. Additionally, a KIAA1247 homologue from rat is known as protein from WO 98/53071, whose expression is induced in injured or regenerating tissue, in particular from kidney tissue of the rat. In addition to the known polypeptide from human, the polypeptide from mouse (SEQ ID No. 35) that is mentioned for the first time in this work can also be used. In addition two human splice variants of the gene encoding the polypeptide of SEQ ID No. 36, which are mentioned for the first time in this work, can be used according to the invention. These splice variants encode shorter variants of SEQ ID No. 36: the amino acids 652 to 654 and 664 to 681 or the amino acids 664 to 681 of the polypeptide of SEQ ID No. 36, respectively, are deleted in these variants. In addition, other KIAA1247 polypeptides can be used according to the invention, which result from alternative translation initiation ATG-codon. Examples of such variants are disclosedin WO 00/73454 and in WO 00/58473. Phospholipase inhibitor GIPL from human (SEQ ID No. 38), that is known from U.S. Pat. Nos. 5,948,626, 5,663,059 and 5,811,520. In addition to the already known polypeptide from human the polypeptide from mouse (SEQ ID No. 37), that is

mentioned in this work for the first time, and the closely related polypeptides with a significantly divergent sequence (SEQ ID No. 45 and SEQ ID No. 81), which are mentioned in this work for the first time, can be used. The cDNA encoding the polypeptide according to SEQ ID No. 81 is indicated under SEQ ID No. 84. EAT/MCL-1 from mouse (SEQ ID No. 39) or human (SEQ ID No. 40), that is known from WO 95/28497, which is expressed in numerous tissues (Krajewski et al., 1995, Am. J. Pathol. 146:1309-19) and that plays role in cutaneous malignant melanoma (Tang et al., 1998, Clin. Cancer Res. 4:1865-71). TSC-22 (TGF-beta-stimulated clone 22 gene) from human (SEQ ID No. 42) and mouse (SEQ ID No. 41) (Jay et al., 1996, Biochem. Biophys. Res. Commun. 222:821-826; Shibanuma et al., 1992, J. Biol. Chem. 267:10219-10224), that belongs to the "leucine-zipper" family of transcription factors (Kester et al., 1999, J. Biol. Chem. 274:27439-47). Transcription of TSC-22 is induced by variety of stimuli as, for instance, growth inhibitors (Kester et al., 1999, J. Biol. Chem. 274:27439-47). Additionally an increased expression of TSC-22 during development of the mouse embryo was observed at locations where mesenchymal-epithelial interaction occurs (Dohrmann et al., 1999, Mech. Dev. 84:147-51). Gamma-sarcoglycan from human (SEQ ID No. 44) or mouse (SEQ ID No. 43) (Noguchi et al., 1995, Science 270:819-822; Noguchi et al., 1999, Biochem. Biophy. Res. Commun. 262:88-93), that is known from JP 100 57 065 and U.S. Pat. No. 5,837,537. Gamma-sarcoglycan is a component of the sarcoglycan complex that again is a subcomplex of the dystrophin gycoprotein complex. This establishes a connection between the extracellular matrix and the actin cytoskeleton (Hack et al., 2000, Microsc. Res. Tech. 48:167-80). Mutation of gamma-sarcoglycan has been described as a primary genetic defect of a muscular dystrophy (SCARMD) (Noguchi et al., 1995, Science 270:819-822). Cysteine proteinase inhibitor cystatin C from human (SEQ ID No. 47) or mouse (SEQ ID No. 46) (Abrahamson et al., 1987, FEBS Lett. 216:229-233; Solem et al., 1990, Biochem. Biophys. Res. Commun. 172:945-951), that is known from WO 99/38882, WO 88/09384, DE 372 4 581, JP 012 02 287, JP 010 74 988 and U.S. Pat. No. 5,212,297. Cystein protease inhibitors play a role in inflammatory disorders as, for example, rheumatism (Lenarcic et al., 1988, Biol. Chem. Hoppe Seyler 369 (Suppl.):257-261) and in vascular disorders (Shi et al., 1999, J. Clin. Invest. 104:1191-1197). In addition to the known polypeptide variant from mouse (SEQ ID No. 46) (Solem et al., 1990, Biochem. Biophys. Res. Commun. 172:945-951) the closely related polypeptide with a divergent sequence, that has been described in this work for the first time (SEQ ID No. 48) can also be used. The tyrosine kinase Fer from mouse (SEQ ID No. 63) or human (SEQ ID No. 64) (SwissProt: P70451; Hao et al., 1989, Mol. Cell. Biol. 9:1587-1593), that is both localized in the nucleus as well as in the cytoplasm (Hao et al., 1991, Mol. Cell. Biol. 11:1180-1183). A role for Fer has been postulated both for cell-cell-adhesion (Rosato et al., 1998, Mol. Cell. Biol. 18:5762-5770) as well as a role as proto-oncogen (Morris et al., 1990, Cytogenet. Cell. Genet. 53:196-200). The C-C cytokine MRP-3 (macrophage inflammatory protein 3) from mouse (SEQ ID No. 65) or human (SEQ ID No. 66), that is known from WO 99/28473, WO 96/34891 and WO 98/14582, that is also called C10, MPIF-1 (Myeloid Progenitor Inhibitory Factor-1), CK-beta-8 or small inducible cytokine A23 (Orlosfsky et al., 1991, Cell Regul. 2:403-412; Li and Ruben, 1996, U.S. Pat. No. 5,504,003). A high expression of MRP-3 a macrophages has been observed in chronic infection of the peritoneum (Wu et al., 1999, Cytokine 11:523-30). As a typical C-C cytokine MRP-3 is a chemoattractant for leukocytes (Haelens et al., 1996, Immunobiology 195:499-521) but it also effects osteoclasts (Votta et al., 2000, J. Cell

Physiol. 183:196-207). In addition it has been observed that MRP-3 mRNA is not significantly upregulated by stimuli, that are connected to wound healing (Orlofsky et al., Cell Regul., 1991, 2:403-412). The nicotinamide **N-methyltransferase** NNMT from mouse (SEQ ID No. 67) or human (SEQ ID No. 68) (Aksoy et al., 1994, J. Biol. Chem. 269:14835-14840; Yan et al., 1997, Biochem. Pharmacol. 54:1139-1149), that catalyzes the methyltransfer of S-adenosylmethionine to nicotineamide. There are several pieces of evidence, that NNMT can regulate the growth of liver cells (Seifert et al., 1984, Biochim, Biophys. Acta 801:259-64). In addition a role of the enzyme in liver cancer has been proposed (Hoshino et al., Biochim. Biophys. Acta 719:518-526). The ubiquitin protein ligase UBC9 from mouse (SEQ ID No. 69) or human (SEQ ID No. 70) (Yasugi and Howley; 1996, Nucleic Acids Res. 24:2005-2010; SwissProt: P50550), that is an important component of the proteasome mediated protein degradation (Hershko and Ciechanover, 1998, Annu. Rev. Biochem. 67:425-479). The ubiquitin dependent protein degradation plays a role in most divergent processes like cell cycle control, signal transduction or immune response. There are indications that UBC9 plays a role in accelerated aging (Kawabe et al., 2000, J. Biol. Chem.). In addition UBC9 catalyzes the sumoylation of p53 and thus **activates its function as transcription** factor (Rodriguez et al., 1999, EMBO J. 18:6455-61).

US-PAT-NO: 6583275

DOCUMENT-IDENTIFIER: US 6583275 B1

TITLE: Nucleic acid sequences and expression system relating to Enterococcus faecium for diagnostics and therapeutics

DATE-ISSUED: June 24, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Doucette-Stamm; Lynn A.	Framingham	MA	N/A	N/A
Bush; David	Somerville	MA	N/A	N/A

APPL-NO: 09/ 107532

DATE FILED: June 30, 1998

PARENT-CASE:

This application claims priority of U.S. provisional applications No. 60/051,571, filed Jul. 2, 1997; and No. 60/085,598 filed May 14, 1998, all of which are hereby incorporated herein by reference in their entirety.

US-CL-CURRENT: 536/23.1, 435/243 , 435/320.1 , 435/325 , 435/6 , 536/24.3 , 536/24.32

ABSTRACT:

The invention provides isolated polypeptide and nucleic acid sequences derived Enterococcus faecium that are useful in diagnosis and therapy of pathological conditions; antibodies against the polypeptides; and methods for the production of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

34 Claims, 0 Drawing figures

Exemplary Claim Number: 1

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Detailed Description Paragraph Table - DETL (68):
[le:53481] [re:53684] [di:direct] 33683327_c1_52 2361 6015 987 328 607 2.80E-59 [ac:p37517] [gn:yyag] [or:bacillus subtilis] [de:hypothetical transcriptional regulator in tetb-exoa intergenic region] [sp:p37517] [db:swissprot] 3368837_c1_48 2362 6016 966 321 850 4.90E-85 [ac:p46469] [gn:ftsh:trna] [or:lactococcus lactis] [sr:,subsplactis:streptococcus lactis]

[ec:3.4.24.--] [de:cell division protein ftsh homolog,] [sp:p46469]
[db:swissprot] 3370462_c1_28 2363 6017 1440 479 1422 1.20E-145 [ln:bsaraabd]
[ac:x89408] [pn:1-arabinose isomerase] [gn:araa] [or:bacillus subtilis]
[db:genpept-bct] [de:b.subtilis dna for araa, arab and arad genes.] [le:228]
[re:1718] [di:direct] 33710307_c3_16 2364 6018 1464 487 1813 4.40E-187
[ln:af008553] [ac:af008553] [pn:glu-trnagln amidotransferase subunit b]
[gn:gatb] [or:bacillus subtilis] [db:genpept-bct] [de:bacillus subtilis
glu-trnagln amidotransferase subunits c (gatc), a (gata) and b (gatb) genes,
complete cds.] [le:2185] [re:3615] 33710333_c3_31 2365 6019 1044 347 81
0.011 [ac:p34859] [gn:nd41] [or:apis mellifera] [sr:,honeybee] [ec:1.6.5.3]
[de:nadh-ubiquinone oxidoreductase chain 41,] [sp:p34859] [db:swissprot]
33750955_c2_70 2366 6020 3660 1219 107 4.40E-05 [ac:p54509] [gn:yqhh]
[or:bacillus subtilis] [de:hypothetical helicase in sini-gcvt intergenic
region] [sp:p54509] [db:swissprot] 33756517_f3_22 2367 6021 417 138 60 0.35
[ac:p21536] [gn:atp8] [or:schizosaccharomyces pombe] [sr:,fission yeast]
[ec:3.6.1.34] [de:atp synthase protein 8, (a61)] [sp:p21536] [db:swissprot]
3376717_c3_49 2368 6022 297 98 87 0.002 [ac:s36779:s36780]
[pn:ribosome-binding protein p34] [cl:leucine-rich alpha-2-glycoprotein
repeat homology] [or:rattus norvegicus] [sr:, norway rat] [db:pir]
33773427_f3_80 2369 6023 927 308 190 5.50E-13 [ac:p77672] [gn:ydey]
[or:escherichia coli] [de:hypothetical abc transporter permease protein ydey]
[sp:p77672] [db:swissprot] 33776465_f1_2 2370 6024 231 77 192 1.50E-14
[ac:q47745] [gn:vansb] [or:enterococcus faecalis] [sr:,streptococcus faecalis]
[ec:2.7.3.--] [de:protein vansb) (vancomycin histidine protein kinase)]
[sp:q47745] [db:swissprot] 33788280_c1_118 2371 6025 768 255 102 0.021
[ac:p75563] [gn:phet] [or:mycoplasma pneumoniae] [ec:6.1.1.20] [de:trna
ligase beta chain) (phers)] [sp:p75563] [db:swissprot] 33789187_c3_72 2372
6026 513 170 61 0.41 [ac:q44148] [or:anabaena sp] [sr:pcc 7120,]
[de:hypothetical 8.2 kd protein in nifx-nifw intergenic region (orf1)]
[sp:q44148] [db:swissprot] 33790813_c3_19 2373 6027 1125 374 1351 4.00E-138
[ac:p37572] [gn:rada:sms] [or:bacillus subtilis] [de:dna repair protein rada
homolog (dna repair protein sms homolog)] [sp:p37572] [db:swissprot]
33791088_c1_48 2374 6028 2031 676 244 8.40E-20 [ac:p32058] [gn:cmtb]
[or:escherichia coli] [ec:2.7.1.69] [de:enzyme ii, a component),] [sp:p32058]
[db:swissprot] 33792553_c2_152 2375 6029 531 176 92 0.0082 [ac:i41076]
[pn:**methyltransferase** m.ecohk31i beta chain] [or:escherichia coli] [db:pir]
33798177_f2_22 2376 6030 855 284 767 3.10E-76 [ac:e69742] [pn:abc transporter
(atp-binding protein) homolog ybae] [gn:ybae] [or:bacillus subtilis] [db:pir]
33804712_c3_46 2377 6031 207 68 105 9.40E-06 [ac:p36942] [gn:gpmb]
[or:escherichia coli] [ec:5.4.2.1] [de:2) (pgam 2) (bpg-dependent pgam 2)]
[sp:p36942] [db:swissprot] 33828175_c2_24 2378 6032 222 73 62 0.068
[ln:cet21b4] [ac:z81124] [pn:t21b4.8] [or:caenorhabditis elegans]
[db:genpept-inv] [de:caenorhabditis elegans cosmid t21b4, complete sequence.]
[nt:similar to 7tm receptor] [le:24866:25711:25952] [re:25339:25901:26294]
[di:complementjoin] 33828175_f1_12 2379 6033 1077 358 94 0.11 [ac:p36044]
[gn:yk1200c] [or:saccharomyces cerevisiae] [sr:,baker's yeast]
[de:hypothetical 46.9 kd protein in tor2-pas1 intergenic region] [sp:p36044]
[db:swissprot] 33828175_f3_21 2380 6034 216 71 54 0.67 [ln:pbu42580]
[ac:u42580:u17055:u32570] [gn:a3091] [or:paramecium bursaria chlorella virus
1] [db:genpept-vrl] [de:paramecium bursaria chlorella virus 1, complete
genome.] [le:155062] [re:155298] [di:complement] 33828175_f3_7 2381 6035 324
107 57 0.41 [ac:i77320] [pn:nadh dehydrogenase subunit 5] [or:mitochondrion
lemur catta] [sr:, ring-tailed lemur] [db:pir] 33828450_c1_47 2382 6036 465

154 193 2.10E-15 [ac:e69786] [pn:ribosomal-protein-alanine n-acetyltransfer homolog ydid] [gn:ydid] [or:bacillus subtilis] [db:pir] 33829037_f1_18 2383 6037 1797 598 700 3.90E-69 [ac:g69815] [pn:abc transporter (atp-binding protein) homolog ygad] [gn:ygad] [or:bacillus subtilis] [db:pir] 33833442_c2_20 2384 6038 204 67 71 0.069 [ln:u88974] [ac:u88974] [pn:orf9] [or:streptococcus thermophilus] [db:genpept-bct] [de:streptococcus thermophilus bacteriophage 01205 dna sequence.] [nt:contains a putaive atp/gtp binding site between] [le:4086] [re:4787] [di:direct] 33834555_c1_20 2385 6039 345 115 53 0.84 [ln:hiv192610] [ac:z92610] [pn:gp120, c2/v3 region] [gn:env] [or:human immunodeficiency virus type 1] [db:genpept-vrl] [de:human immunodeficiency virus type 1 env gene (strain kr45-1).] [le:<1] [re: 33835937_c3_58 2386 6040 1131 376 1441 1.20E-147 [ac:p37518] [gn:yyaf] [or:bacillus subtilis] [de:region] [sp:p37518] [db:swissprot] 33835961_f2_2 2387 6041 321 107 177 1.30E-13 [ac:p96314] [gn:prfb] [or:bacillus firmus] [de:peptide chain release factor 2 (rf-2) (fragment)] [sp:p96314] [db:swissprot] 33838290_c2_64 2388 6042 342 113 109 4.40E-06 [ln:af016485] [ac:af016485] [or:halobacterium sp. nrc-1] [db:genpept-bct] [de:halobacterium sp. nrc-1 plasmid pnrc100, complete plasmid sequence.] [nt:orfh0801] [le:72330] [re:73046] [di:complement] 33844635_f2_4 2389 6043 213 71 75 0.24 [ac:s75142] [pn:sensory transduction histidine kinase:protein slr1759:protein slr1759] [or:synechocystis sp.] [sr:pcc 6803, , pcc 6803] [sr:pcc 6803,] [db:pir] 33859377_f3_5 2390 6044 195 64 55 0.19 [ln:af003003] [ac:af003003] [pn:mal63-13p] [gn:mal63] [or:saccharomyces cerevisiae] [sr:baker's yeast] [db:genpept-pln] [de:saccharomyces cerevisiae mal63-13p (mal63) gene, allele ma163-13,complete cds.] [nt:**transcription activator,** nonfunctional mutant] 33859818.sub.-- c1_36 2391 6045 234 77 68 0.13 [ac:q16763] [or:homo sapiens] [sr:,human] [ec:6.3.2.19] [de:protein ligase) (ubiquitin carrier protein) (e2-epf5)] [sp:q16763] [db:swissprot] 33860142_c1_58 2392 6046 234 77 70 0.12 [ln:hsp70bg] [ac:x51758] [pn:heat shock protein 70b' (aa 355-643)] [or:homo sapiens] [sr:human] [db:genpept-pri1] [de:human mrna for heat shock protein hsp70b'.] [sp:p17066] [le:<1] [re:870] [di:direct] 33860452_c3_154 2393 6047 2127 708 91 0.029 [ln:cezk945] [ac:z48544] [pn:zk945.10] [or:caenorhabditis elegans] [db:genpept-inv] [de:caenorhabditis elegans cosmid zk945, complete sequence.] [nt:similar to mucin] [sp:q09625] [le:25174:25897:26027] [re:25742:25975:26658] [di:complementjoin] 33861260_c2_48 2394 6048 225 74 50 0.33 [ac:i40591] [pn:arginine--trna ligase,] [gn:args] [or:buchnera aphidicola] [ec:6.1.1.19] [db:pir] 33867817_c1_92 2395 6049 1035 344 1068 3.90E-108 [ac:f70019] [pn:nifs protein homolog homolog yurw] [gn:yurw] [or:bacillus subtilis] [db:pir] 33870692_c3_39 2396 6050 999 332 916 5.00E-92 [ac:h69979] [pn:proteinase homolog yrro] [gn:yrro] [or:bacillus subtilis] [db:pir] 33870712_c2_17 2397 6051 222 73 68

US-PAT-NO: 6576819

DOCUMENT-IDENTIFIER: US 6576819 B1

TITLE: Methods for modulating the levels of organic sulfur compounds in plants by transforming with (P)APS reductase DNA

DATE-ISSUED: June 10, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Leustek; Thomas	Union	NJ	N/A	N/A

APPL-NO: 09/ 252319

DATE FILED: February 18, 1999

US-CL-CURRENT: 800/320, 435/419 , 800/278 , 800/298

ABSTRACT:

Methods for modulating levels of at least one organic sulfur compound in plants are provided. Also provided are plants, plant seeds, and plant cells produced by the methods. The methods comprise stably transforming a plant with a DNA construct encoding at least one APS reductase enzyme or PAPS reductase enzyme (herein, "(P)APS reductase") so that the transformed plant exhibits altered levels of at least one organic sulfur compound. APS reductase is an enzyme classified as EC 1.8.4.9 and PAPS reductase is an enzyme classified as EC 1.8.99.4; these enzymes are capable of reducing sulfur in the form of APS or PAPS to produce sulfite. Also provided are methods for reducing oxidative stress in plants and for increasing the nutritional quality of plants and seeds.

22 Claims, 1 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 1

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Other Reference Publication - OREF (24):

Gary, J. et al., "The Predominant Protein-**arginine Methyltransferase** from Saccharomyces cerevisiae,", Journal of Biological Chemistry, 1996, pp. 12585-12594, vol. 271(21), The American Society for Biochemistry and Molecular Biology, Inc., USA.

US-PAT-NO: 6562958

DOCUMENT-IDENTIFIER: US 6562958 B1

TITLE: Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics

DATE-ISSUED: May 13, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Breton; Gary	Marlborough	MA	N/A	N/A
Bush; David	Somerville	MA	N/A	N/A

APPL-NO: 09/ 328352

DATE FILED: June 4, 1999

PARENT-CASE:

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/088,701, filed Jun. 9, 1998, the entire teachings of which are incorporated herein by reference.

US-CL-CURRENT: 536/23.7, 536/23.1

ABSTRACT:

The invention provides isolated polypeptide and nucleic acid sequences derived from Acinetobacter mirabilis that are useful in diagnosis and therapy of pathological conditions; antibodies against the polypeptides; and methods for the production of the polypeptides. The invention also provides methods for the detection, prevention and treatment of pathological conditions resulting from bacterial infection.

15 Claims, 0 Drawing figures

Exemplary Claim Number: 1

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Detailed Description Paragraph Table - DETL (55):

[DE:DNAK SUPPRESSOR PROTEIN] [SP:P18274] Contig092G 25595275_f1_21 1300 5426 1326 441 1141 9.00E-116 sp:[LN:DHOM_PSEAE] [AC:P29365] [GN:HOM] [OR:PSEUDOMONAS AERUGINOSA] [EC:1.1.1.3] [DE:HOMOSERINE DEHYDROGENASE, (HDH)] [SP:P29365] Contig092G 258_c2_180 1301 5427 495 164 397 6.20E-37

sp:[LN:YCHJ_HAEIN] [AC:P44609] [GN:H10277] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN H10277] [SP:P44609] Contig092G 26843753_f2_74 1302 5428 1434 477 1153 4.80E-117 pir:[LN:S26601] [AC:S33674:S26601] [PN:**transcription activator** pilR] [CL:nitrogen assimilation regulatory protein ntrC:response regulator homology:RNA polymerase sigma factor interaction domain homology] [OR:Pseudomonas aeruginosa] Contig092G 29464153_c2_192 1303 5429 1062 353 534 1.90E-51 sp:[LN:PBP5_PSEAE] [AC:P72161] [GN:PBPG] [OR:PSEUDOMONAS AERUGINOSA] [EC:3.4.99.--] [DE:ENDOPEPTIDASE), (DD- ENDOPEPTIDASE)] [SP:P72161] Contig092G 31796917_f2_73 1304 5430 771 256 614 6.30E-60 gp:[GI:g472403] [LN:PSEMETH] [AC:L29642] [PN:response regulator/**transcription activator**] [OR:Pseudomonas fluorescens] [SR:Pseudomonas fluorescens (strain BL915) DNA] [DE:Pseudomonas fluorescens **methyltransferase** gene, sensor kinase gene, phosphatidylglycerophosphat e synthse (pgsA) gene, UVR excinucleasesubunit C (uvrC) gene, response regulator/transcription activatorgene, complete cds.] [NT:homology with uvrY of E. coli and gacA of P.] Contig092G 3182827_c1_173 1305 5431 741 246 570 2.90E-55 sp:[LN:ALGR_PSEAE] [AC:P26275] [GN:ALGR] [OR:PSEUDOMONAS AERUGINOSA] [DE:POSITIVE ALGINATE BIOSYNTHESIS REGULATORY PROTEIN] [SP:P26275] Contig092G 31910816_f1_46 1306 5432 339 112 NO-HIT Contig092G 33694512_c2_179 1307 5433 1620 539 1193 2.80E-121 pir:[LN:F64972] [AC:F64972] [PN:hypothetical protein b2063] [OR:Escherichia coli] Contig092G 3376637_c2_175 1308 5424 2439 812 1425 3.60E-148 sp:[LN:YGIQ_ECOLI] [AC:Q46861] [GN:YGIQ] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 46.9 KD PROTEIN IN METC-SUFI INTERGENIC REGION] [SP:Q46861] Contig092G 3412750_f2_87 1309 5435 399 132 NO-HIT Contig092G 34265631_c2_190 1310 5436 1119 372 420 2.30E-39 sp:[LN:YJGP_ECOLI] [AC:P39340] [GN:YJGP] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL 40.4 KD PROTEIN IN PEPA-GNTV INTERGENIC REGION (O366)] [SP:P39340] Contig092G 3526587_c2_184 1311 5437 375 124 482 6.10E-46 gp:[GI:g2735324] [LN:AVU91902] [AC:U91902] [PN:PII-protein] [GN:glnB] [OR:Azotobacter vinelandii] [DE:Azotobacter vinelandii PII- protein (glnB) and methylammoniumtransport protein (amtB) genes, complete cds.] Contig092G 35272812_c3_218 1312 5438 1476 491 495 2.60E-47 pir:[LN:G69825] [AC:G69825] [PN:transcription regulator GntR family homolog yhdI] [GN:yhdI] [CL:hypothetical protein b1439] [OR:Bacillus subtilis] Contig092G 35820917_c2_195 1313 5439 1902 633 1654 3.90E-170 gp:[GI:g3128348] [LN:AF010496] [AC:AF010496] [PN:ferrous iron transport protein b] [OR:Rhodobacter capsulatus] [DE:Rhodobacter capsulatus strain SB1003, partial genome.] Contig092G 36211402_f2_64 1314 5440 831 276 441 1.40E-41 sp:[LN-ICC_HAEIN] [AC:P44685] [GN:ICC:H10399] [OR:HAEMOPHILUS INFLUENZAE] [DE:ICC PROTEIN HOMOLOG] [SP:P44685] Contig092G 36348800_c1_141 1315 5441 243 80 NO-HIT Contig092G 36538892_c1_144 1316 5442 420 139 151 7.30E-11 sp:[LN:YBBI_ECOLI] [AC:P77565] [GN:YBBI] [OR:ESCHERICHIA COLI] [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN USHA-TESA INTERGENIC REGION] [SP:P77565] Contig092G 3906542_f3_132 1317 5443 363 120 235 9.10E-20 gp:[GI:g2407234] [LN:AF017750] [AC:AF017750] [GN:hypol 17] [OR:Haemophilus ducreyi] [DE:Haemophilus ducreyi cytochrome C-type biogenesis protein (ccmH), recombinational DNA repair protein (rccR), manganese superoxidedismutase (sodA), and CitG protein homolog (citG) genes, completecds.] [NT:simiiar to Haemophilus influenzae product encoded] Contig092G 3990718_f1_109 1318 5444 825 274 376 1.00E-34 gp:[GI:g3135321] [LN:AF057031] [AC:AF057031] [PN:putative thiol:disulfide interchange protein]

[GN:dsbC] [OR:Pseudomonas aeruginosa] [DE:Pseudomonas aeruginosa putative thiol:disulfide

US-PAT-NO: 6558935

DOCUMENT-IDENTIFIER: US 6558935 B1

TITLE: Human transferase proteins

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Tang; Y. Tom	San Jose	CA	N/A	N/A
Corley; Neil C.	Castro Valley	CA	N/A	N/A
Guegler; Karl J.	Menlo Park	CA	N/A	N/A
Baughn; Mariah R.	San Leandro	CA	N/A	N/A
Lal; Preeti	Santa Clara	CA	N/A	N/A
Yue; Henry	Sunnyvale	CA	N/A	N/A
Hillman; Jennifer L.	Mountain View	CA	N/A	N/A
Azimzai; Yalda	Castro Valley	CA	N/A	N/A

APPL-NO: 09/ 786240

DATE FILED: March 12, 2002

PARENT-CASE:

This application is the national stage entry of PCT/US99/20989, filed Sep. 9, 1999, which claims the benefit of Ser. No. 60/172,220, filed Sep. 10, 1998, U.S. Ser. No. 60/155,248, filed Nov. 4, 1998, and U.S. Ser. No. 60/133,642, filed May 11, 1999.

PCT-DATA:
APPL-NO: PCT/US99/20989
DATE-FILED: September 9, 1999
PUB-NO: WO00/14251
PUB-DATE: Mar 16, 2000
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 435/193, 435/252.3 , 435/252.33 , 435/320.1 , 435/325 , 435/91.1 , 530/350 , 536/23.1 , 536/23.2 , 536/23.5

ABSTRACT:

The invention provides human transferase proteins (TRNSFS) and polynucleotides which identify and encode TRNSFS. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provide methods for diagnosing, treating, or preventing disorders, associated with expression of TRNSFS.

5 Claims, 6 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 6

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Brief Summary Text - BSTX (13):

The enzyme glycine N-**methyltransferase** catalyzes the transfer of the methyl group from S-adenosyimethionine to glycine to form S-adenosylhomocteine and sarcosine. Glycine N-**methyltransferase** is a tetramer of identical subunits, has a nucloetide binding region, and is localized in the liver. Amino acid sequence homology is found between glycine N-methlytransferases from rat, rabbit, pig, and human livers. Glycine N-**methyltransferase** can exist as a dimer which binds polycyclic aromatic hydrocarbons (PAHs) and acts as a **transcriptional activator** (Ogawa, H. et al. (1998) Int. J. Biochem. Cell Biol. 30:13-26; Bhat, R. and Bresnick, E. (1997) J. Biol. Chem. 272:21221-21226).

US-PAT-NO: 6534261

DOCUMENT-IDENTIFIER: US 6534261 B1

TITLE: Regulation of endogenous gene expression in cells using zinc finger proteins

DATE-ISSUED: March 18, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cox, III; George Norbert	Louisville	CO	N/A	N/A
Case; Casey Christopher	San Mateo	CA	N/A	N/A
Eisenberg; Stephen P.	Boulder	CO	N/A	N/A
Jarvis; Eric Edward	Boulder	CO	N/A	N/A
Spratt; Sharon Kaye	Vacaville	CA	N/A	N/A

APPL-NO: 09/ 229037

DATE FILED: January 12, 1999

PARENT-CASE:

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to co-owned patent application entitled "Selection of Sites for Targeting by Zinc Finger Proteins and Methods of Designing Zinc Finger Proteins to Bind to Pre-selected Sites," U.S. Ser. No. 09/229,007,filed Jan. 12, 1999, herein incorporated by reference in its entirety.

US-CL-CURRENT: 435/6, 435/29 , 536/23.5 , 536/24.1

ABSTRACT:

The present invention provides methods for modulating expression of endogenous cellular genes using recombinant zinc finger proteins.

85 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 8

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Detailed Description Text - DETX (28):

A "**transcriptional activator" and a "transcripti nal** repressor" refer to

proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detailed Description Text - DETX (77):

Common regulatory domains for addition to the ZFP include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

US-PAT-NO: 6528289

DOCUMENT-IDENTIFIER: US 6528289 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

DATE-ISSUED: March 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Fleischmann; Robert D.	Gaithersburg	MD	N/A	N/A
Adams; Mark D.	N. Potomac	MD	N/A	N/A
White; Owen	Gaithersburg	MD	N/A	N/A
Smith; Hamilton O.	Towson	MD	N/A	N/A
Venter; J. Craig	Potomac	MD	N/A	N/A

APPL-NO: 09/ 643990

DATE FILED: August 23, 2000

PARENT-CASE:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of application Ser. No. 08/487,429, filed Jun. 7, 1995 which is a continuation-in-part of application Ser. No. 08/426,787, filed Apr. 21, 1995, now abandoned, which is hereby incorporated by reference.

US-CL-CURRENT: 435/91.41, 435/252.3 , 435/320.1 , 435/6 , 536/23.1 , 536/23.7

ABSTRACT:

The present invention provides the sequencing of the entire genome of Haemophilus influenzae Rd, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies over 1700 protein encoding fragments of the genome and identifies, by position relative to a unique Not I restriction endonuclease site, any regulatory elements which modulate the expression of the protein encoding fragments of the Haemophilus genome.

23 Claims, 47 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 47

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Detailed Description Paragraph Table - DETL (5):
nitrogenase regulator (modD) 31.8 51.7 259 [Rhodobacter capsulatus] HI0200 214274 215227 msbB protein (msbB) [Escherichia coli] 45.3 67.0 301 HI0411 429238 430662 msbB protein (msbB) [Escherichia coli] 50.9 69.3 284 HI0712 756824 757117 negative regulator of translation (relB) [Escherichia coli] 28.3 48.3 60 HI0631 667822 668406 negative rpo regulator (mclA) [Escherichia coli] 20.1 62.9 199 HI0269 299532 301232 nitrate sensor protein (narQ) [Escherichia coli] 38.6 63.0 555 HI0728 778003 777380 nitrate/nitrite response regulator protein (narP) [Escherichia coli] 59.6 79.3 205 HI0339 363915 364250 nitrogen regulatory protein P-II (glnB) [Escherichia coli] 77.7 93.8 112 HI1747 1828067 1826037 penta-phosphate guanosine-3'-pyrophosphohydrolase (spoT) [Escherichia 58.8 76.6 675 coli] HI1381 1475017 1473741 phosphate regulon sensor protein (phoR) [Escherichia coli] 41.8 66.8 335 HI1382 1475709 1475017 phosphate regulon transcriptional regulatory protein (phoB) [Escherichia 52.9 71.8 227 coli] HI0765 827030 825768 probable nadAB transcriptional regulator (nadR) [Escherichia coli] 54.6 75.1 349 HI1641 1697003 1698115 purine nucleotide synthesis repressor protein (purR) [Escherichia coli] 55.9 74.5 328 HI0164 178405 178713 putative murein gene regulator (bolA) [Escherichia coli] 47.1 65.7 102 HI0508 522278 523273 rps repressor (rbsR) [Escherichia coli] 48.8 71.0 329 HI0565 582225 581776 regulatory protein (asnC) [Escherichia coli] 68.0 81.0 147 HI1617 1677452 1676583 regulatory protein sfs1 involved in maltose metabolism (sfsA) [Escherichia 54.3 71.2 218 coli] HI0895 946128 946688 repressor for cytochrome P450 (Bm3R1) [Bacillus megaterium] 23.3 50.6 182 HI0271 302396 303238 RNA polymerase sigma-32 factor (heat shock regulatory protein F334) 70.8 86.8 281 (rpoH) [Escherichia coli] HI0535 555646 557532 RNA polymerase sigma-70 factor (rpoD) [Escherichia coli] 68.9 80.8 608 HI0630 667228 667794 RNA polymerase sigma-E factor (rpoE) [Escherichia coli] 73.0 87.8 189 HI1713 1781137 1779785 sensor protein for basR (basS) [Escherichia coli] 30.0 55.7 253 HI1444 1529117 1528668 stringent starvation protein (sspB) [Escherichia coli] 63.2 81.1 106 HI1445 1529755 1529120 stringent starvation protein A (sspA) [Haemophilus somnus] 76.9 87.3 212 HI1745 1815630 1814704 trans-activator of metE and metH (metR) [Escherichia coli] 39.5 60.8 294 HI0360 382477 383121 **transcription activator** (tenA) [Bacillus subtilis] 27.8 48.3 208 HI0683 722643 721768 **transcriptional activator** protein (ilvY) [Escherichia coli] 47.4 70.3 293 HI1714 1781799 1781137 transcriptional regulatory protein (basR) [Escherichia coli] 43.5 59.7 216 HI0412 430780 431733 transcriptional regulatory protein (tyrR) [Escherichia coli] 48.2 66.8 306 HI0832 880611 880913 tryptophan repressor (trpR) [Enterobacter aerogenes] 39.8 67.0 88 HI0054 54188 54985 uxu operon regulator (uxuR) [Escherichia coli] 50.0 72.1 246 HI1109 1170415 1169255 xylose operon regulatory protein (xylR) [Escherichia coli] 57.3 75.3 384 Replication DNA-replication, restr/modification, recombination HI0761 822003 823136 A/G-specific adenine glycosylase (mutY) [Escherichia coli] 61.6 75.1 341 HI0995 1056674 1055313 chromosomal replication initiator protein (dnaA) [Escherichia coli] 61.7 79.7 464 HI1229 1294415 1294317 chromosomal replication initiator protein (dnaA) [Escherichia coli] 50.0 75.0 12 HI0316 345720 345151 crossover junction endodeoxyribonuclease (ruvC) [Escherichia coli] 78.5 88.3 163 HI0955 1011537 1012736 dip protein (dfp) [Escherichia coli] 61.1 76.8 402 HI0210 223259

224116 DNA adenine methylase (dam) [Escherichia coli] 55.4 71.4 266 HI1267 1343755 1341116 DNA gyrase, subunit A (gyrA) [Escherichia coli] 70.6 84.9 859 HI0569 587397 584980 DNA gyrase, subunit B (gyrB) [Escherichia coli] 74.7 85.9 803 HI1191 1255302 1253122 DNA helicase II (uvrD) [Haemophilus influenzae] 96.8 97.5 727 HI1102 1162989 1160953 DNA ligase (lig) [Escherichia coli] 63.7 79.9 666 HI0405 423539 424207 DNA mismatch protein (mutH) [Escherichia coli] 60.4 80.7 212 HI0709 750565 753147 DNA mismatch repair protein (mutS) [Escherichia coli] 71.0 84.0 853 HI0067 69622 71508 DNA mismatch repair protein MUTL (mutL) [Escherichia coli] 50.2 67.3 612 HI0858 904919 902130 DNA polymerase I (polA) [Escherichia coli] 63.1 77.0 928 HI0994 1055297 1054200 DNA polymerase III beta-subunit (dnaN) [Escherichia coli] 62.6 80.3 366 HI0457 476761 475763 DNA polymerase III delta prime subunit (holB) [Escherichia coli] 35.3 57.4 316 HI0925 979730 980761 DNA polymerase III delta subunit (holA) [Escherichia coli] 45.2 62.0 332 HI0138 152669 151902 DNA polymerase III epsilon subunit (dnaQ) [Escherichia coli] 61.3 76.5 236 HI0741 799019 795544 DNA polymerase III, alpha chain (dnaE) [Escherichia coli] 71.9 85.7 1159 HI1402 1493690 1493259 DNA polymerase III, chi subunit (holC) [Haemophilus influenzae] 98.9 98.9 88 HI0011 11672 11271 DNA polymerase III, psi subunit (holD) [Escherichia coli] 34.4 59.2 123 HI0534 553659 555645 DNA primase (dnaG) [Escherichia coli] 56.5 73.8 571 HI1746 1826037 1823959 DNA recombinase (recG) [Escherichia coli] 66.5 80.1 693 HI0070 77166 75493 DNA repair protein (recN) [Escherichia coli] 48.6 67.3 533 HI0659 699507 700058 DNA topoisomerase I (topA) [Bacillus subtilis] 34.2 55.0 110 HI0656 698124 697570 DNA-3-methyladenine glycosidase I (tagI) [Escherichia coli] 62.6 76.0 179 HI0730 779457 781969 DNA-dependent ATPase, DNA helicase (recQ) [Escherichia coli] 62.9 77.6 589 HI0568 584860 584159 dod protein (dod) [Serratia marcescens] 81.4 93.3 210 HI0062 65230 65664 dosage-dependent dnaK supressor protein (dksA) [Escherichia coli] 73.9 83.8 142 HI0948 1005798 1004986 formamidopyrimidine-DNA glycosylase (fpg) [Escherichia coli] 57.6 74.7 269 HI0584 602405 600519 glucose inhibited division protein (gidA) [Escherichia coli] 76.1 87.3 627 HI0488 506816 506208 glucose inhibited division protein (gidB) [Escherichia coli] 64.0 78.0 200 HI0982 1037496 1037792 Hin recombinational enhancer binding protein (fis) [Escherichia coli] 81.6 92.9 97 HI0514 528338 527565 HincII endonuclease (HincII) [Haemophilus influenzae] 98.4 98.4 258 HI1397 1491189 1490263 HindIII modification **methyltransferase** (hindIIIM) [Haemophilus influenzae] 99.4 99.4 309 HI1398 1492072 1491173 HindIII restriction endonuclease (hindIIIR) [Haemophilus influenzae] 99.7 99.7 300 HI0315 345085 344474 holiday junction DNA helicase (ruvA) [Escherichia coli] 58.8 79.9 203 HI0314 344463 343459 holiday junction DNA helicase (ruvB) [Escherichia coli] 80.9 90.0 330 HI0678 719064 718180 integrase/recombinase protein (xerC) [Escherichia coli] 58.0 74.4 293 HI1316 1391102 1391389 integration host factor alpha-subunit (himA) [Escherichia coli] 63.8 83.0 94 HI1224 1291400 1291681 integration host factor beta-subunit (IHF-beta (himD) [Escherichia coli] 56.5 77.2 92 HI0404 422970 423539 methylated-DNA-protein-cysteine **methyltransferase** (dat1) [Bacillus 40.1 61.7 163 subtilis] HI0671 713369 713806 mioC protein (mioC) [Escherichia coli] 53.5 71.5 144 HI1043 1104813 1105724 modification methylase MHgiDI (MHgiDI) [Herpetosiphon aurantiacus] 56.4 70.5 297 HI0515 529891 528338 modification methylase HincII (hincIIM) [Haemophilus influenzae] 98.2 98.6 502 HI0912 963611 964312 mutator mutT (AT-GC transversion) [Escherichia coli] 48.8 72.0 125 HI0193 206098 206688 negative modulator of initiation of replication (seqA) [Escherichia coli] 53.1 71.8 177 HI0548 568202 567879 primosomal protein n precursor (priB) [Escherichia coli] 57.4 75.2 101 HI0341 367532

365343 primosomal protein replication factor (priA) [Escherichia coli] 52.3 70.2 729 HI0389 406402 708321 probable ATP-dependent helicase (dinG) [Escherichia coli] 32.2 51.1 680 HI0993 1054243 1053119 recF protein (recF) [Escherichia coli] 57.0 75.8 356 HI0334 358532 359239 recO protein (recO) [Escherichia coli] 64.6 76.5 226 HI0602 621957 620896 recombinase (recA) [Haemophilus influenzae] 100.0 100.0 354 HI0061 64971 62573 recombination protein (rec2) [Haemophilus influenzae] 99.9 99.9 800 HI0445 464118 464717 recR protein (recR) [Escherichia coli] 74.9 88.4 199 HI0601 620735 620358 regulatory protein (recX) [Pseudomonas fluorescens] 28.6 20.4 117 HI0651 694862 692768 rep helicase (rep) [Escherichia coli] 66.9 82.7 669 HI1232 1299240 1297177 replication protein (dnaX) [Escherichia coli] 52.9 69.8 643 HI1580 1641089 1642600 replicative DNA helicase (dnaB) [Escherichia coli] 68.6 82.8 462 HI1042 1103812 1104813 restriction enzyme (hgiDIR) [Herpetosiphon giganteus] 44.2 63.9 350 HI1175 1241423 1242574 S-adenosylmethionine synthetase 2 (metX) [Escherichia coli] 82.3 91.7 383 HI1429 1512463 1511552 shufflon-specific DNA recombinase (fci) [Escherichia coli] 31.1 55.5 259 HI0251 281830 282333 single-stranded DNA binding protein (ssb) [Haemophilus influenzae] 95.8 98.2 168 HI1578 1639113 1638016 site-specific recombinase (rcb) [Escherichia coli] 36.3 57.0 265 HI1368 1450325 1452928 topoisomerase I (topA) [Escherichia coli] 72.0 84.3 865 HI0446 464736 466688 topoisomerase III (topB) [Escherichia coli] 65.9 79.4 645 HI1535 1599641 1601882 topoisomerase IV subunit A (parC) [Escherichia coli] 71.4 85.4 727 HI1534 1597676 1599571 topoisomerase IV subunit B (parE) [Escherichia coli] 76.5 88.6 630 HI1261 1331575 1335011 transcription-repair coupling factor (trcF) (mfd) [Escherichia coli] 64.3 82.7 1134 HI0217 232884 234038 type I restriction enzyme ecokI specificity protein (hsdS) [Escherichia coli] 36.1 58.6 394 HI0216 231281 232797 type I restriction enzyme ECOR124/3 I M protein (hsdM) [Escherichia coli] 81.2 89.3 512 HI1290 1368549 1367223 type I restriction enzyme ECOR124/3 I M protein (hsdM) [Escherichia coli] 30.4 53.7 332 HI1288 1365756 1362592 type I restriction enzyme ECOR124/3 R protein (hsdR) [Escherichia coli] 30.4 52.7 991 HI1059 1123091 1121205 type III restriction-modification ECOP15 enzyme (mod) [Escherichia coli] 36.5 55.5 384 HI0018 18087 18743 uracil DNA glycosylase (ung) [Escherichia coli] 70.2 79.5 215 HI0311 342051 342941 xprB protein (xerD) [Escherichia coli] 68.9 84.8 296 Degradation of DNA HI1695 1758680 1759312 endonuclease III (nth) [Escherichia coli] 83.4 91.9 211 HI0250 278528 281829 excinuclease ABC subunit A (uvrA) [Escherichia coli] 81.2 91.0 940 HI1250 1323924 1321888 excinuclease ABC subunit B (uvrB) [Escherichia coli] 78.0 87.7 669 HI0057 58893 57067 excinuclease ABC subunit C (uvrC) [Escherichia coli] 65.9 80.0 588 HI1380 1471626 1473044 exodeoxyribonuclease I (sbcB) [Escherichia coli] 57.5 74.9 462 HI1324 1395898 1399530 exodeoxyribonuclease V (recB) [Escherichia coli] 37.1 58.2 1165 HI0944 998895 1002257 exodeoxyribonuclease V (recC) [Escherichia coli] 40.1 61.2 1114 HI1325 1399533 1401452 exodeoxyribonuclease V (recD) [Escherichia coli] 40.0 59.3 570 HI0041 43872 43072 exonuclease III (xthA) [Escherichia coli] 71.9 83.9 267 HI0399 417972 419288 exonuclease VII, large subunit (xseA) [Escherichia coli] 57.8 74.4 437 HI1217 1280795 1282519 single-stranded-DNA-specific exonuclease (recJ) [Escherichia coli] 59.2 77.3 554 Transcription RNA synthesis, modification and DNA transcription HI0618 647724 650492 ATP-dependent helicase HEPA (hepA) [Escherichia coli] 53.6 73.6 968 HI0424 444751 443435 ATP-dependent RNA helicase (srmB) [Escherichia

US-PAT-NO: 6506581

DOCUMENT-IDENTIFIER: US 6506581 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

DATE-ISSUED: January 14, 2003

INVENTOR-INFORMATION:

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Fleischmann; Robert D.	Gaithersburg	MD	N/A	N/A
Adams; Mark D.	N. Potomac	MD	N/A	N/A
White; Owen	Gaithersburg	MD	N/A	N/A
Smith; Hamilton O.	Towson	MD	N/A	N/A
Venter; J. Craig	Potomac	MD	N/A	N/A

APPL-NO: 09/ 557884

DATE FILED: April 25, 2000

PARENT-CASE:

This application is a continuation of U.S. application Ser. No. 08/476,102, filed Jun. 7, 1995, which is a continuation-in-part of U.S. application Ser. No. 08/426,787, filed Apr. 21, 1995, now abandon.

US-CL-CURRENT: 435/69.1, 435/252.3 , 435/320.1 , 435/69.3 , 435/91.41 , 536/23.7

ABSTRACT:

The present invention provides the sequencing of the entire genome of Haemophilus influenzae Rd, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies over 1700 protein encoding fragments of the genome and identifies, by position relative to a unique Not I restriction endonuclease site, any regulatory elements which modulate the expression of the protein encoding fragments of the Haemophilus genome.

51 Claims, 47 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 47

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Detailed Description Paragraph Table - DETL (5):

HI1617 1677452 1676583 regulatory protein sfs1 involved in maltose metabolism (sfsA) [Escherichia coli] 54.3 71.2 218 HI0895 946128 946688 repressor for cytochrome P450 (Bm3R1) [Bacillus megaterium] 23.3 50.6 182 HI0271 302396 303238 RNA polymerase sigma-32 factor (heat shock regulatory protein F334) (rpoH) 70.8 86.8 281 [Escherichia coli] HI0535 555646 557532 RNA polymerase sigma-70 factor (rpoD) [Escherichia coli] 68.9 80.8 608 HI0630 667228 667794 RNA polymerase sigma-E factor (rpoE) [Escherichia coli] 73.0 87.8 189 HI1713 1781137 1779785 sensor protein for basR (basS) [Escherichia coli] 30.0 55.7 253 HI1444 1529117 1528668 stringent starvation protein (sspB) [Escherichia coli] 63.2 81.1 106 HI1445 1529755 1529120 stringent starvation protein A (sspA) [Haemophilus somnus] 76.9 87.3 212 HI1745 1815630 1814704 trans-activator of metE and metH (metR) [Escherichia coli] 39.5 60.8 294 HI0360 382477 383121 **transcription activator** (tenA) [Bacillus subtilis] 27.8 48.3 208 HI0683 722643 721768 **transcriptional activator** protein (ilvY) [Escherichia coli] 47.4 70.3 293 HI1714 1781799 1781137 transcriptional regulatory protein (basR) [Escherichia coli] 43.5 59.7 216 HI0412 430780 431733 transcriptional regulatory protein (tyrR) [Escherichia coli] 48.2 66.8 306 HI0832 880611 880913 tryptophan repressor (trpR) [Enterobacter aerogenes] 39.8 67.0 88 HI0054 54188 54985 uxu operon regulator (uxuR) [Escherichia coli] 50.0 72.1 246 HI1109 1170415 1169255 xylose operon regluatory protein (xylR) [Escherichia coli] 57.3 75.3 384 Replication DNA - replication, restr/modification, recombination HI0761 822003 823136 A/G-specific adenine glycosylase (mutY) [Escherichia coli] 61.6 75.1 341 HI0995 1056674 1055313 chromosomal replication initiator protein (dnaA) [Escherichia coli] 61.7 79.7 464 HI1229 1294415 1294317 chromosomal replication initiator protein (dnaA) [Escherichia coli] 50.0 75.0 12 HI0316 345720 345151 crossover junction endodeoxyribonuclease (ruvC) [Escherichia coli] 78.5 88.3 163 HI0955 1011537 1012736 dfp protein (dfp) [Escherichia coli] 61.1 76.8 402 HI0210 223259 224116 DNA adenine methylase (dam) [Escherichia coli] 55.4 71.4 266 HI1267 1343755 1341116 DNA gyrase, subunit A (gyrA) [Escherichia coli] 70.6 84.9 859 HI0569 587397 584980 DNA gyrase, subunit B (gyrB) [Escherichia coli] 74.7 85.9 803 HI1191 1255302 1253122 DNA helicase II (uvrD) [Haemophilus influenzae] 96.8 97.5 727 HI1102 1162989 1160953 DNA ligase (lig) [Escherichia coli] 63.7 79.9 666 HI0405 423539 424207 DNA mismatch protein (mutH) [Escherichia coli] 60.4 80.7 212 HI0709 750565 753147 DNA mismatch repair protein (mutS) [Escherichia coli] 71.0 84.0 853 HI0067 69622 71508 DNA mismatch repair protein MUTL (mutL) [Escherichia coli] 50.2 67.3 612 HI0858 904919 902130 DNA polymerase I (polA) [Escherichia coli] 63.1 77.0 928 HI0994 1055297 1054200 DNA polymerase III beta-subunit (dnaN) [Escherichia coli] 62.6 80.3 366 HI0457 476761 475763 DNA polymerase III delta prime subunit (holB) [Escherichia coli] 35.3 57.4 316 HI0925 979730 980761 DNA polymerase III delta subunit (holA) [Escherichia coli] 45.2 62.0 332 HI0138 152669 151902 DNA polymerase III epsilon subunit (dnaQ) [Escherichia coli] 61.3 76.5 236 HI0741 799019 795544 DNA polymerase III, alpha chain (dnaE) [Escherichia coli] 71.9 85.7 1159 HI1402 1493690 1493259 DNA polymerase III, chi subunit (holC) [Haemophilus influenzae] 98.9 98.9 88 HI0011 11672 11271 DNA polymerase III, psi subunit (holD) [Escherichia coli] 34.4 59.2 123 HI0534 553659 555645 DNA primase (dnaG) [Escherichia coli] 56.5 73.8 571 HI1746 1826037 1823959 DNA recombinase (recG) [Escherichia coli] 66.5 80.1 693 HI0070 77166 75493 DNA repair protein (recN) [Escherichia coli] 48.6 67.3 533 HI0659 699507 700058 DNA topoisomerase I (topA) [Bacillus subtilis] 34.2 55.0 110 HI0656 698124

697570 DNA-3-methyladenine glycosidase I (tagI) [Escherichia coli] 62.6 76.0 179 HI0730 779457 781969 DNA-dependent ATPase, DNA helicase (recQ) [Escherichia coli] 62.9 77.6 589 HI0568 584860 584159 dod protein (dod) [Serratia marcescens] 81.4 93.3 210 HI0062 65230 65664 dosage-dependent dnaK suppressor protein (dksA) [Escherichia coli] 73.9 83.8 142 HI0948 1005798 1004986 formamidopyrimidine-DNA glycosylase (fpg) [Escherichia coli] 57.6 74.7 269 HI0584 602405 600519 glucose inhibited division protein (gldA) [Escherichia coli] 76.1 87.3 627 HI0488 506816 506208 glucose inhibited division protein (gldB) [Escherichia coli] 64.0 78.0 200 HI0982 1037496 1037792 Hin recombinational enhancer binding protein (fis) [Escherichia coli] 81.6 92.9 97 HI0514 528338 527565 HincII endonuclease (HincII) [Haemophilus influenzae] 98.4 98.4 258 HI1397 1491189 1490263 HindIII modification **methyltransferase** (hindIIIM) [Haemophilus influenzae] 99.4 99.4 309 HI1398 1492072 1491173 HindIII restriction endonuclease (hindIIIR) [Haemophilus influenzae] 99.7 99.7 300 HI0315 345084 344474 holliday junction DNA helicase (ruvA) [Escherichia coli] 58.8 79.9 203 HI0314 344463 343459 holliday junction DNA helicase (ruvB) [Escherichia coli] 80.9 90.0 330 HI0678 719064 718180 integrase/recombinase protein (xerC) [Escherichia coli] 48.0 74.4 293 HI1316 1391102 1391389 integration host factor alpha-subunit (himA) [Escherichia coli] 63.8 83.0 94 HI1224 1291400 1291681 integration host factor beta-subunit (IHF-beta) (himD) [Escherichia coli] 56.5 77.2 92 HI0404 422970 423539 methylated-DNA--protein-cysteine **methyltransferase** (dat1) [Bacillus subtilis] 40.1 61.7 163 HI0671 713369 713806 mioC protein (mioC) [Escherichia coli] 53.5 71.5 144 HI1043 1104813 1105724 modification methylase HgiDI (MHgiDI) [Herpetosiphon aurantiacus] 56.4 70.5 297 HI0515 529891 528338 modification methylase HincII (hincIIM) [Haemophilus influenzae] 98.2 98.6 502 HI0912 963611 964312 mutator mutT (AT-GC transversion) [Escherichia coli] 58.8 72.0 125 HI0193 206098 206688 negative modulator of initiation of replication (seqA) [Escherichia coli] 53.1 71.8 177 HI0548 568202 567879 primosomal protein n precursor (priB) [Escherichia coli] 57.4 75.2 101 HI0341 367532 365343 primosomal protein replication factor (priA) [Escherichia coli] 52.3 70.2 729 HI0389 406402 408321 probable ATP-dependent helicase (dinG) [Escherichia coli] 32.2 51.1 680 HI0993 1054243 1053119 recF protein (recF) [Escherichia coli] 57.0 75.8 356 HI0334 358532 359239 recO protein (recO) [Escherichia coli] 64.6 76.5 226 HI0602 621957 620896 recombinase (recA) [Haemophilus influenzae] 100.0 100.0 354 HI0061 64971 625573 recombination protein (rec2) [Haemophilus influenzae] 99.9 99.9 800 HI0445 464118 464717 recR protein (recR) [Escherichia coli] 74.9 88.4 199 HI0601 620735 620358 regulatory protein (recX) [Pseudomonas fluorescens] 28.6 50.4 117 HI0651 694862 692768 rep helicase (rep) [Escherichia coli] 66.9 82.7 669 HI1232 1299240 1297177 replication protein (dnaX) [Escherichia coli] 52.9 69.8 643 HI1580 1641089 1642600 replicative DNA helicase (dnaB) [Escherichia coli] 68.6 82.8 462 HI1042 1103812 1104813 restriction enzyme (hgiDIR) [Herpetosiphon giganteus] 44.2 63.9 350 HI1175 1241423 1242574 S-adenosylmethionine synthetase 2 (metX) [Escherichia coli] 82.3 91.7 383 HI1429 1512463 1511552 shufflon-specific DNA recombinase (rci) [Escherichia coli] 31.1 55.5 259 HI0251 281830 282333 single-stranded DNA binding protein (ssb) [Haemophilus influenzae] 95.8 98.2 168 HI1578 1639113 1638016 site-specific recombinase (rcb) [Escherichia coli] 36.3 57.0 265 HI1368 1450325 1452928 topoisomerase I (topA) [Escherichia coli] 72.0 84.3 865 HI0446 464736 466688 topoisomerase III (topB) [Escherichia coli] 65.9 79.4 645 HI1535 1599641 1601881 topoisomerase IV subunit A (parC) [Escherichia coli] 71.4 85.4 727 HI1534 1597676 1599571 topoisomerase IV subunit B (parE) [Escherichia coli] 76.5 88.6

630 HI1261 1331575 1335011 transcription-repair coupling factor (trcF) (mfd) [Escherichia coli] 64.3 82.7 1134 HI0217 232884 234038 type I restriction enzyme ecokI specificity protein (hsdS) [Escherichia coli] 36.1 58.6 394 HI0216 231281 232797 type I restriction enzyme ECOR124/3 I M protein (hsdM) [Escherichia coli] 81.2 89.3 512 HI1290 1368549 1367223 type I restriction enzyme ECOR124/3 I M protein (hsdM) [Escherichia coli] 30.4 53.7 332 HI1288 1365756 1362592 type I restriction enzyme ECOR124/3 R protein (hsdR) [Escherichia coli] 30.4 52.7 991 HI1059 1123091 1121205 type III restriction-modification ECOP15 enzyme (mod) [Escherichia coli] 36.5 55.5 384 HI0018 18087 18743 uracil DNA glycosylase (ung) [Escherichia coli] 70.2 79.5 215 HI0311 342051 342941 xprB protein (xerD) [Escherichia coli] 68.9 84.8 296 Degradation of DNA HI1695 1758680 1759312 endonuclease III (nth) [Escherichia coli] 83.4 91.9 211 HI0250 278528 281829 excinuclease ABC subunit A (uvrA) [Escherichia coli] 81.2 91.0 940 HI1250 1323924 1321888 excinuclease ABC subunit B (uvrB) [Escherichia coli] 78.0 87.7 669 HI0057 58893 57067 excinuclease ABC subunit C (uvrC) [Escherichia coli] 65.9 80.0 588 HI1380 1471626 1473044 exodeoxyribonuclease I (sbcB) [Escherichia coli] 57.5 74.9 462 HI1324 1395898 1399530 exodeoxyribonuclease V (recB) [Escherichia coli] 37.1 58.2 1165 HI0944 998895 1002257 exodeoxyribonuclease V (recC) [Escherichia coli] 40.1 61.2 1114 HI1325 1399533 1401452 exodeoxyribonuclease V (recD) [Escherichia coli] 40.0 59.3 570 HI0041 43872 43072 exonuclease III (xthA) [Escherichia coli] 71.9 83.9 267 HI0399 417972 419288 exonuclease VII, large subunit (xseA) [Escherichia coli] 57.8 74.4 437 HI1217 1280795 1282519 single-stranded-DNA-specific exonuclease (recJ) [Escherichia coli] 59.2 77.3 554 Transcription RNA synthesis, modification and DNA transcription HI0618 647724 650492 ATP-dependent helicase HEPA (hepA) [Escherichia coli] 53.6 73.6 968 HI0424 444751 443435 ATP-dependent RNA helicase (srmB) [Escherichia coli] 39.8 60.9 448 HI0232 260978 262816 ATP-dependent RNA helicase DEAD (deaD) [Escherichia coli] 64.0 78.6 613 HI0804 851485 852468 DNA-directed RNA polymerase alpha chain (ropA) [Escherichia coli] 91.8 97.0 329 HI0517 534212 538870 DNA-directed RNA polymerase beta chain (rpoB) [Salmonella typhimurium] 83.3 91.9 1342 HI0516 534211 529967 DNA-directed RNA polymerase beat' chain (rpoC) [Escherichia coli] 83.0 90.7 1399 HI1307 1383078 1383509 N utilizatin substance protein B (nusB) [Escherichia coli] 54.9 71.4 133 HI0063 65915 67269 plasmid copy number control protein (pcnB) [Escherichia coli] 55.7 73.4 404 HI0230 257702 259828 polynucleotide phosphorylase (pnp) [Escherichia coli] 74.2 86.7 708 HI0894 944630 945883 putative ATP-dependent RNA helicase (rhlB) [Escherichia coli] 73.9 84.1 410 HI1748 1828594 1828331 RNA polymerase omega subunit (rpoZ) [Escherichia coli] 64.8 76.1 88 HI1463 1542205 1541624 sigma factor (algU) [Pseudomonas aeruginosa] 27.6 48.8 168 HI0719 764847 765401 transcription antitermination protein (nusG) [Escherichia coli] 73.7 84.4 179 HI0571 589932 590405 transcription elongation factor (greB) [Escherichia coli] 61.5 79.5 156 HI1286 1358486 1360006 transcription factor (nusA) [Salmonella typhimurium] 70.8 84.1 499 HI0297 328437 329696 transcription termination factor rho (rho) [Escherichia coli] 87.4 95.2 419 Degradation of RNA HI0219 234848 237923 anticodon nuclease masking-agent (prrD) [Escherichia coli] 72.9 85.6 291 HI1739 1810586 1808610 exoribonuclease II (RNaseII) [Escherichia coli] 50.8 68.0 588 HI0392 411354 412550 ribonuclease D (md) [Escherichia coli] 41.3 65.5 365

US-PAT-NO: 6503717

DOCUMENT-IDENTIFIER: US 6503717 B2

TITLE: Methods of using randomized libraries of zinc finger proteins for the identification of gene function

DATE-ISSUED: January 7, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Case; Casey C.	San Mateo	CA	N/A	N/A
Liu; Qiang	Foster City	CA	N/A	N/A
Rebar; Edward J.	El Cerrito	CA	N/A	N/A
Wolffe; Alan P.	Orinda	CA	N/A	N/A

APPL-NO: 09/ 731558

DATE FILED: December 6, 2000

PARENT-CASE:

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to U.S. Ser. No. 09/229,007, filed Jan. 12, 1999, and U.S. Ser. No. 09/229,037, filed Jan. 12, 1999, and U.S. Ser. No. 09/395,448, filed Sep. 14, 1999, herein each incorporated by reference in their entirety.

US-CL-CURRENT: 435/6, 435/320.1 , 435/455 , 536/23.5

ABSTRACT:

The present invention relates to methods of using libraries of randomized zinc finger proteins to identify genes associated with selected phenotypes.

30 Claims, 5 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 5

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Detailed Description Text - DETX (7):

In one embodiment, the zinc finger protein is linked to at least one or more regulatory domains, described in detail below. Preferred regulatory domains

include **transcription fact r repressor or activator** domains such as KRAB and VP16, co-repressor and co-activator domains, DNA **methyltransferases,** histone acetyltransferases, histone deacetylases, and endonucleases such as Fok1. For repression of gene expression, often simple steric hindrance of transcription initiation is sufficient.

Detailed Description Text - DETX (24):

A "**transcriptional activator" and a "transcriptional** repressor" refer to proteins or effector domains of proteins that have the ability to modulate transcription, as described above. Such proteins include, e.g., transcription factors and co-factors (e.g., KRAB, MAD, ERD, SID, nuclear factor kappa B subunit p65, early growth response factor 1, and nuclear hormone receptors, VP16, VP64), endonucleases, integrases, recombinases, **methyltransferases,** histone acetyltransferases, histone deacetylases etc. Activators and repressors include co-activators and co-repressors (see, e.g., Utley et al., Nature 394:498-502 (1998)).

Detailed Description Text - DETX (53):

Common regulatory domains for addition to the zinc finger protein include, e.g., effector domains from **transcription factors (activators,** repressors, co-activators, co-repressors), silencers, nuclear hormone receptors, oncogene transcription factors (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers.

US-PAT-NO: 6500938

DOCUMENT-IDENTIFIER: US 6500938 B1

TITLE: Composition for the detection of signaling pathway gene expression

DATE-ISSUED: December 31, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Au-Young; Janice	Berkeley	CA	N/A	N/A
Seilhamer; Jeffrey J.	Los Altos Hills	CA	N/A	N/A

APPL-NO: 09/ 016434

DATE FILED: January 30, 1998

US-CL-CURRENT: 536/23.1, 422/50 , 422/68.1 , 435/6 , 436/501 , 536/24.1 , 536/24.3 , 536/24.31 , 536/24.32 , 536/24.33

ABSTRACT:

The present invention relates to a composition comprising a plurality of polynucleotide probes. The composition can be used as array elements in a microarray. The present invention also relates to a method for selecting polynucleotide probes of the composition.

5 Claims, 0 Drawing figures

Exemplary Claim Number: 1

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Detailed Description Paragraph Table - DETL (10):

[human.] SEQ ID NO: 938 779308 180141 cell surface antigen. [human.] SEQ ID NO: 939 779596 1017721 Human repressor transcriptional factor (ZNF85) mRNA, complete cds. [human.] SEQ ID NO: 940 782996 186512 Homo sapiens 19 (clone.2) interferon-gamma IEF 51 SSP mRNA [Homo sapiens cDNA to mRNA.] SEQ ID NO: 941 785643 340458 DNA-binding protein. [human.] SEQ ID NO: 942 787082 1699163 ETX1 [alternatively spliced] [human, retina, 4 Peptide, aa]. [human retina.] SEQ ID NO: 943 791011 2072014 phosphatidylinositol-4-phosphate-5-kinase. [domestic pig.] SEQ ID NO: 944 791681 311337 stimulatory GTP binding protein. [dog.] SEQ ID NO: 945 796012 163225 inositol monophosphatase. [cow.] SEQ ID NO: 946 796375 498730 H. sapiens HZF6 mRNA for zinc finger protein. [human.] SEQ ID NO: 947 805552 193402 GABA-alpha receptor delta-subunit. [house mouse.] SEQ ID NO: 948 807267 1617117 H. sapiens mRNA for thiol-specific antioxidant. [human.] SEQ ID NO: 949 810389 495567 Human zinc finger protein (ZNF139)

mRNA, partial cds. [human.] SEQ ID NO: 950 819550 1020091 neuropsin. [house mouse.] SEQ ID NO: 951 820694 532504 stratum corneum chymotryptic enzyme. [human.] SEQ ID NO: 952 824265 487840 Zinc finger. [human.] SEQ ID NO: 953 827431 2077932 Protein Kinase. [Norway rat.] SEQ ID NO: 954 828082 442421 Human **activating transcription** factor 3 (ATF3) mRNA, complete cds. [Homo sapiens cDNA to mRNA.] SEQ ID NO: 955 832067 1657265 Human DNA sequence from 179 PAC, between markers DXS6791 and [human.] SEQ ID NO: 956 834251 1136337 leucine-zipper protein. [chicken.] SEQ ID NO: 957 835995 340450 DNA-binding protein. [human.] SEQ ID NO: 958 836623 459152 RANTES. [Norway rat.] SEQ ID NO: 959 837890 1050529 H. sapiens ZNF74-1 mRNA. [human.] SEQ ID NO: 960 838332 1199603 Human zinc finger protein C2H2-25 mRNA, complete cds. [human.] SEQ ID NO: 961 839651 453373 zinc finger protein. [house mouse.] SEQ ID NO: 962 841903 1644377 H. sapiens ICAAR gene. [human.] SEQ ID NO: 963 842889 532032 Homo sapiens (subclone 6 H8 from P1 35 H5 C8) DNA sequence. [Homo sapiens (library: Subclones in pSP72 from P1 clone 35 H5 C8] SEQ ID NO: 964 850121 56392 R. norvegicus mRNA for H36-alpha7 integrin alpha chain. [Norway rat.] SEQ ID NO: 965 851571 498730 H. sapiens HZF6 mRNA for zinc finger protein. [human.] SEQ ID NO: 966 852401 189677 Human protein C inhibitor gene, complete cds. [Homo sapiens DNA.] SEQ ID NO: 967 852708 1655624 H. sapiens mRNA for arginine **methyltransferase.** [human.] SEQ ID NO: 968 857279 1314667 CfOLF4. [dog.] SEQ ID NO: 969 858552 1066920 E03A3.2. [Caenorhabditis elegans.] SEQ ID NO: 970 859876 1857636 Human phosphatidylinositol-4-phosphate 5-kinase type II beta mRNA, [human.] SEQ ID NO: 971 859906 1753102 Human putative G protein-coupled receptor (GPR20) gene, complete [human.] SEQ ID NO: 972 861034 1209875 Rattus norvegicus Myx mRNA, complete cds. [brown rat.] SEQ ID NO: 973 862023 1695802 Human MOP3 mRNA, complete cds. [human.] SEQ ID NO: 974 862403 567206 growth factor. [house mouse.] SEQ ID NO: 975 864259 2145059 Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds. [human.] SEQ ID NO: 976 864272 531750 probable mitochondrial protein. [baker's yeast.] SEQ ID NO: 977 864414 288344 R. norvegicus mRNA for inhibitory glycine receptor alpha 2A subunit. [Norway rat.] SEQ ID NO: 978 864683 575361 protein kinase PkpA. [Phycomyces blakesleeanus.] SEQ ID NO: 979 865569 1040966 Rattus rattus PCTAIRE-1 protein kinase mRNA, alternatively spliced, [black rat.] SEQ ID NO: 980 866123 829619 protein kinase [Arabidopsis thaliana] SEQ ID NO: 981 866390 1314665 CfOLF3. [dog.] SEQ ID NO: 982 873352 1695172 member of PDGF/VEGT family of growth factors. [house mouse.] SEQ ID NO: 983 876063 56392 R. norvegicus mRNA for H36-alpha7 integrin alpha chain. [Norway rat.] SEQ ID NO: 984 877555 56493 Rat mRNA for integrin alpha-1. [Norway rat.] SEQ ID NO: 985 877705 340486 DNA-binding protein. [human.] SEQ ID NO: 986 877928 1161343 interleukin 17 receptor. [house mouse.] SEQ ID NO: 987 878146 1151256 transmembrane receptor. [house mouse.] SEQ ID NO: 988 878906 902886 Ksp-cadherin [Oryctolagus cuniculus] SEQ ID NO: 989 881694 189940 Human phosphorylase kinase (PSK-C3) mRNA, complete cds. [Human HeLa cell line, cDNA to mRNA.] SEQ ID NO: 990 881996 2145079 Homo sapiens TGF-beta related neurotrophic factor receptor 2 [human.] SEQ ID NO: 991 882035 2149603 Mus musculus flotillin mRNA, complete cds. [house mouse.] SEQ ID NO: 992 884071 1150862 Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, [Norway rat.] SEQ ID NO: 993 889096 1777755 protein tyrosine phosphatase PTPCAAX1. [human.] SEQ ID NO: 994 889949 841318 mutant sterol regulatory element binding protein [Cricetulus griseus] SEQ ID NO: 995 896136 1430822 Ste20-like kinase. [human.] SEQ ID NO: 996 897147 1769577 A6 protein tyrosine kinase homolog. [house mouse.] SEQ ID NO: 997 898537 1813876 smoothened. [human.] SEQ ID NO: 998

898651 2160295 protein tyrosine-serine-threonine kinase. [thale cress.] SEQ ID NO: 999 899024 180990 Human cytoplasmic phosphtyrosine phosphatase mRNA. [Homo sapiens placenta cDNA to mRNA.] SEQ ID NO: 1000 899043 1613847 Human zinc finger protein zfp6 (ZF6) mRNA, partial cds. [human.] SEQ ID NO: 1001 902631 38031 Human ZNF43 mRNA. [human.] SEQ ID NO: 1002 907157 1835659 multidrug resistance-associated protein. [human.] SEQ ID NO: 1003 915403 1236650 PP-1M. [Norway rat.] SEQ ID NO: 1004 917525 307328 Human protocadherin 43 mRNA, complete cds for abbreviated PC43. [Homo sapiens (tissue library: Stratagene) brain cDNA to mRNA.] SEQ ID NO: 1005 924579 1890117 Homo sapiens casein kinase I gamma 2 mRNA, complete cds. [human.] SEQ ID NO: 1006 924778 49941 M. musculus mRNA for AM2 receptor. [house mouse.] SEQ ID NO: 1007 926018 1086452 MAP kinase kinase. [fruit fly.] SEQ ID NO: 1008 926034 1836161 Ca2+/calmodulin-dependent protein kinase IV kinase isoform, [Rattus sp. brain.] SEQ ID NO: 1009 926250 387675 protocadherin 42. [human.] SEQ ID NO: 1010 926642 205106 Rat neuronal delayed rectifier K+ channel (K-V-4) mRNA, complete [Rattus norvegicus (strain Sprague-Dawley) brain cDNA to mRNA.] SEQ ID NO: 1011 927003 202806 vasopressin receptor. [Norway rat.] SEQ ID NO: 1012 927740 263348 zinc finger = ZNF126 [human, Peptide Partial, 98 aa]. [human.] SEQ ID NO: 1013 928085 1913900 Human 236 clones 237 and zinc finger protein mRNA, complete [human.] SEQ ID NO: 1014 928596 206189 protein kinase C type II. [Norway rat.] SEQ ID NO: 1015 928762 488557 zinc finger protein ZNF137. [human.] SEQ ID NO: 1016 929130 487736 putative potassium channel subunit. [fruit fly.] SEQ ID NO: 1017 930839 163783 transducin beta subunit. [cow.] SEQ ID NO: 1018 932340 1707017 RNA helicase isolog. [thale cress.] SEQ ID NO: 1019 933230 529400 transcription regulator. [house mouse.] SEQ ID NO: 1020 934370 1835659 multidrug resistance-associated protein. [human.] SEQ ID NO: 1021 937019 1617517 orphan G protein-coupled receptor. [human.] SEQ ID NO: 1022 937525 498727 zinc finger protein. [human.] SEQ ID NO: 1023 938735 602434 GABA/noradrenaline transporter. [human.] SEQ ID NO: 1024 939088 28638 Human mRNA for antileukoprotease (ALP) from cervix uterus. [human.] SEQ ID NO: 1025 939531 1373393 Human zinc finger protein (LD5-1) mRNA, complete cds. [human.] SEQ ID NO: 1026 947336 56392 R. norvegicus mRNA for H36-alpha7 integrin alpha chain. [Norway rat.] SEQ ID NO: 1027 949299 1916230 granulocyte chemotactic protein-2. [human.] SEQ ID NO: 1028 954226 1813563 paraxis. [chicken.] SEQ ID NO: 1029 956818 1468943 AEBP1. [human.] SEQ ID NO: 1030 959745 2072185 Human osteoprotegerin (OPG) protein, complete sequence.#. [human.] SEQ ID NO: 1031 961450 32455 H. sapiens hR-PTPu gene for protein tyrosine phosphatase. [human.] SEQ ID NO: 1032 965175 1752644 Rat mRNA for NB-3, complete cds. [Rattus norvegicus (strain: Wistar) brain cDNA to mRNA.] SEQ ID NO: 1033 965517 1905801 monocyte chemotactic protein-2. [human.] SEQ ID NO: 1034 966470 292936 Human zinc finger mRNA. [Homo sapiens female hippocampus cDNA to mRNA.] SEQ ID NO: 1035 968129 984304 serine/threonine kinase PAK homolog DPAK [Homo sapiens] SEQ ID NO: 1036 968249 338477 Human zinc finger protein (SRE-ZBP) mRNA, 3' end. [Homo sapiens cDNA to mRNA.] SEQ ID NO: 1037 971090 256854 nek1 = serine/threonine- and tyrosine-specific protein kinase [mice, [Mus sp. erythroleukemia cells.] SEQ ID NO: 1038 975377 1304598 Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking [human.] SEQ ID NO: 1039 980625 1022773 Mus musculus transcription factor TFEB mRNA, partial cds. [house mouse strain =

US-PAT-NO: 6492168

DOCUMENT-IDENTIFIER: US 6492168 B1

TITLE: Methyltransferase gene and enzyme

DATE-ISSUED: December 10, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Kladde; Michael P.	Bryan	TX	N/A	N/A
Simpson; Robert T.	Lemont	PA	N/A	N/A
Xu; Mai	Hangzhou	N/A	N/A	CN

APPL-NO: 09/ 296840

DATE FILED: April 22, 1999

PARENT-CASE:

This application claims priority to U.S. Provisional Application Serial No. 60/082,674, filed Apr. 22, 1998, which is incorporated by reference herein.

Pursuant to 35 U.S.C. .sctn.202(c), it is acknowledged that the U.S. Government has certain rights in the invention described herein, which was made in part with funds from the National Institutes of Health, Grant No. GM52908.

US-CL-CURRENT: 435/325, 435/252.3 , 435/254.1 , 435/320.1 , 435/410 , 435/455 , 435/468 , 435/471 , 536/23.1 , 536/23.2 , 536/23.72 , 536/24.33

ABSTRACT:

A novel cytosine-5 DNA methyltransferase, isolated from Chlorella virus NYs-1, and its encoded enzyme are disclosed. The methyltransferase recognizes a GpC dinucleotide in DNA. Methods of using the novel methyltransferase in high resolution chromatin mapping and related techniques are also disclosed.

16 Claims, 6 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 4

---------- KWIC ---------

Brief Summary Text - BSTX (5):

In vivo methylation of DNA has been used successfully to study protein-DNA

interactions in the chromatin of living cells. A high frequency of **methyltransferase** targets is critical for high resolution mapping of chromatin structure. Among currently available **methyltransferase** probes, the only de novo dinucleotide **methyltransferase** is M.SssI, which recognizes a CpG site (Renbaum, P., Abrahamove, D., Fainsod, A., Wilson, G., Rottem, S. and Razin, A. (1990) Nucleic Acids Res., 18, 1145-1152). Due to under-representation of the CpG dinucleotide in the genome, the resolution of chromatin structure maps using this enzyme is about 35 base pairs on average in S. cerevisiae (Dujon, B., Alexandrakl, D., Andre, B., Ansorge, W., Baladron, V., Ballesta, J. P. G., Banrevl, A., Bolle, P. A., Bolotin-Fukuhara, M., Bossler, P. et al). (1994) Nature, 369, 371-378.). With this moderate level of resolution, M.SssI can possibly serve to detect the presence of a positioned nucleosome, 146 bp in yeast, without the need for introduction of additional CpG sites into native DNA sequences. However, this resolution is insufficient for mapping the interactions of non-histone regulatory proteins, since the typical length of the target DNA sequence of most regulatory proteins is .about.20-30 base pairs or less. For example, the yeast TATA box binding protein (TBP) recognizes and binds to an 8 bp sequence (Kim, Y., Geiger, J. H., Hahn, S. and Sigler, P. B. (1993) Nature, 365, 512-520.), while the well-characterized **transcriptional activator** Gal4p binds to a 17 bp consensus sequence (Giniger, E., Varnum, S. M. and Ptashne, M. (1985) Cell, 40, 767-774.). Furthermore, methylation of CpG islands has been implicated as an important controlling element for gene regulation in mammalian systems, which may limit the application of M.SssI in higher organisms (Tazi, J. and Bird, A. (1990) Cell, 60, 909-920.). To address both the limitation of resolution and the possible inability to utilize M.SssI in higher organisms, cloning and expression of cytosine-5-DNA **methyltransferases** (5-.sup.me C MTase) with different specificities but similarly small recognition sites is essential.

US-PAT-NO: 6471959

DOCUMENT-IDENTIFIER: US 6471959 B1

TITLE: Human transferase

DATE-ISSUED: October 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Lal; Preeti	Santa Clara	CA	N/A	N/A
Bandman; Olga	Mountain View	CA	N/A	N/A
Hillman; Jennifer L.	Mountain View	CA	N/A	N/A
Guegler; Karl J.	Menlo Park	CA	N/A	N/A
Gorgone; Gina A.	Boulder Creek	CA	N/A	N/A
Corley; Neil C.	Mountain View	CA	N/A	N/A
Patterson; Chandra	Mountain View	CA	N/A	N/A

APPL-NO: 09/ 490032

DATE FILED: January 21, 2000

PARENT-CASE:

This application is a division of application Ser. No. 09/109,204, filed Jun. 30, 1998, now U.S. Pat. No. 6,060,250.

US-CL-CURRENT: 424/94.5, 435/15 , 435/16 , 435/193 , 435/320.1 , 536/23.2

ABSTRACT:

The invention provides three human transferases (HUTRAN) and polynucleotides which identify and encode HUTRAN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating or preventing disorders associated with expression of HUTRAN.

7 Claims, 7 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 7

---------- KWIC ---------

Brief Summary Text - BSTX (7):

Protein-**arginine methyltransferases** catalyze the posttranslational methylation of arginine residues in proteins, resulting in the mono- and

dimethylation of arginine on the guanidino group. Known substrates are histones, heterogeneous nuclear ribonucleoproteins (hnRNPs), and myelin basic protein. This otherwise unusual posttranslational modification is common in hnRNPs and may regulate their function. hnRNPs function in the nucleus in mRNA processing, splicing, and transport into the cytoplasm. Homologous protein-**arginine methyltransferases** that methylate hnRNPs have been cloned from yeast, rat, and man. These protein-**arginine methyltransferases** contain five sequence motifs, termed region I, post-region I, region II, region III, and post-region III, that may be involved in binding S-adenosyl-methionine. One human gene (HRMT1L1) encodes a 433 amino acid protein. The other human gene (HRMT1L2) may be alternatively spliced to yield three protein-**arginine methyltransferases,** of length 343, 347, and 361 amino acids respectively, with different amino termini. The protein encoded by the cloned rat protein-**arginine methyltransferase** gene (PRMT1) interacts with the TIS21 protein and the homologous BTG1 protein. The intermediate-early TIS21 protein is the product of a gene induced by treatment of cells with mitogens such as epidermal growth factor, and the-BTG1 protein is the product of a human gene located near a chromosome translocation breakpoint associated with chronic lymphocytic leukemia. The HRMT1L2 protein interacts with the cytoplasmic domain of the interferon receptor. This interaction suggests that protein methylation may be an important signaling mechanism for cytokine receptors (Lin, W.-J. et al..(1996) J. Biol. Chem. 271:15034-15044; Abramovich, C. et al. (1997) EMBO J. 16:260-266; and Scott, H. S. et al. (1998) Genomics 48:330-340.)

Drawing Description Text - DRTX (4):

FIGS. 3A, 3B, and 3C show the amino acid sequence alignment between HUTRAN-3 (2525071; SEQ ID NO:3) and human **arginine methyltransferase** (GI 1808648; SEQ ID NO:32).

Detailed Description Text - DETX (53):

As shown in Table 2, each HUTRAN has been characterized with regard to its chemical and structural similarity with transferase molecules. As shown in FIGS. 1A and 1B, HUTRAN-1 and human glutamine-phenylpyruvate aminotransferase (GI 758591; SEQ ID NO:30) share 49% identity. As shown in FIGS. 2A and 2B, HUTRAN-2 and rat kynurenine/.alpha.-aminoadipate aminotransferase (GI 1050752; SEQ ID NO:31) share 71% identity. As shown in FIGS. 3A, 3B, and 3C, HUTRAN-3 and human **arginine methyltransferase** (GI 1808648; SEQ D NO:32) share 27% identity.

Detailed Description Text - DETX (91):

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between HUTRAN-1 and glutamine-phenylpyruvate aminotransferase from man (GI 758591), between HUTRAN-2 and kynurenine/.alpha.-aminoadipate aminotransferase from rat (GI 1050752), and between HUTRAN-3 and **arginine methyltransferase** from man (GI 1808648). In addition, HUTRAN is expressed in cancerous, inflamed, male and female reproductive, nervous, and gastrointestinal tissues. Therefore, HUTRAN appears to play a role in autoimmune/inflammatory, neurological, reproductive, and gastrointestinal

disorders, and cancer.

Claims Text - CLTX (1):
1. An isolated polypeptide selected from the group consisting of: a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-3, b) a polypeptide comprising a naturally occurring amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:1, wherein said naturally occurring amino acid sequence has glutamine-phenylpyruvate aminotransferase activity, c) a polypeptide comprising a naturally occurring amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, wherein said naturally occurring amino acid sequence has kynurenine/.alpha.-aminoadipate aminotransferase activity, and d) a polypeptide comprising a naturally occurring amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:3, wherein said naturally occurring amino acid sequence has **arginine methyltransferase** activity.

Other Reference Publication - OREF (9):
Abramovich, C. et al., "A protein-**arginine methyltransferase** binds the intracytoplasmic domain of the IFNAR1 chain in the type I interferon receptor", EMBO J., 16: 260-266 (1997).

Other Reference Publication - OREF (10):
Scott, H.S., et al., "Identification and Characterization of Two Putative Human **Arginine Methyltransferases** (HRMT1L1 and HRMT1L2)", Genomica, 48: 330-340 (1998).

US-PAT-NO: 6453242

DOCUMENT-IDENTIFIER: US 6453242 B1

TITLE: Selection of sites for targeting by zinc finger proteins and methods of designing zinc finger proteins to bind to preselected sites

DATE-ISSUED: September 17, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Eisenberg; Stephen P.	Boulder	CO	N/A	N/A
Case; Casey C.	San Mateo	CA	N/A	N/A
Cox, III; George N.	Louisville	CO	N/A	N/A
Jamieson; Andrew	San Francisco	CA	N/A	N/A
Rebar; Edward J.	Berkeley	CA	N/A	N/A

APPL-NO: 09/ 229007

DATE FILED: January 12, 1999

US-CL-CURRENT: 702/19, 435/6 , 702/20 , 702/21

ABSTRACT:

The invention provides criteria and methods for selecting optimum subsequence(s) from a target gene for targeting by a zinc finger protein. Some of the methods of target site selection seek to identify one or more target segments having a DNA motif containing one or more so-called D-able subsites having the sequence 5'NNGK3'. Other methods of the invention are directed to selection of target segments within target genes using a correspondence regime between different triplets of three bases and the three possible positions of a triplet within a nine-base site. In another aspect, the invention provides methods of designing zinc finger proteins that bind to a preselected target site. These methods can be used following the preselection of target sites according to the procedures and criteria described above. The methods of design use a database containing information about previously characterized zinc finger proteins.

19 Claims, 11 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 10

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Detailed Description Text - DETX (32):

Zinc finger proteins are often expressed with a heterologous domain as fusion proteins. Common domains for addition to the ZFP include, e.g., **transcription fact r d mains (activators,** repressors, co-activators, co-repressors), silencers, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.); DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g. kinases, acetylases and deacetylases); and DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases, endonucleases) and their associated factors and modifiers. A preferred domain for fusing with a ZFP when the ZFP is to be used for represssing expression of a target gene is a the KRAB repression domain from the human KOX-1 protein (Thiesen et al., New Biologist 2, 363-374 (1990); Margolin et al., Proc. Natl. Acad. Sci. USA 91, 4509-4513 (1994); Pengue et al., Nucl. Acids Res. 22:2908-2914 (1994); Witzgall et al., Proc. Natl. Acad. Sci. USA 91, 4514-4518 (1994). Preferred domains for achieving activation include the HSV VP16 activation domain (see, e.g., Hagmann et al., J: Virol. 71, 5952-5962 (1997)) nuclear hormone receptors (see, e.g., Torchia et al., Curr. Opin. Cell Biol. 10:373-383 (1998)); the p65 subunit of nuclear factor kappa B (Bitko & Barik, J Virol. 72:5610-5618 (1998)and Doyle & Hunt, Neuroreport 8:2937-2942 (1997)); Liu et al., Cancer Gene Ther. 5:3-28 (1998)), or artificial chimeric functional domains such as VP64 (Seifpal et al., EMBO J. 11, 4961-4968 (1992)).

US-PAT-NO: 6444421

DOCUMENT-IDENTIFIER: US 6444421 B1

TITLE: Methods for detecting intermolecular interactions in vivo and in vitro

DATE-ISSUED: September 3, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Chung; Jay H.	Bethesda	MD	N/A	N/A

APPL-NO: 09/ 054281

DATE FILED: April 2, 1998

PARENT-CASE:

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. patent application Ser. No. 08/826,622, filed Apr. 3, 1997, which was converted to provisional application Ser. No. 60/080,234 by way of petition filed on Nov. 19, 1997. This application is also related to co-filed U.S. patent application by Jay Chung entitled "Chimeric Endonucleases for Detecting Protein-nucleic Acid Interaction In Vivo and In Vitro," filed Apr. 3, 1997, Ser. No. 08/825,664, which was converted to provisional application Ser No. 60/113,669 by way of petition filed on Nov. 19, 1997, and to co-filed patent application Ser. No. 09/054,231 by Jay Chung entitled "Chimeric Endonucleases For Detecting Intermolecular Interactions In Vivo And In Vitro", filed on Apr. 2, 1998 as These applications are incorporated by reference in their entireties for all purposes.

US-CL-CURRENT: 435/6, 435/455 , 435/69.1 , 435/91.1 , 435/91.3 , 435/91.4

ABSTRACT:

Methods for assessing intermolecular interactions in vivo and in vitro are provided. Methods are provided for detecting protein-DNA interactions in vivo, in which a cell having a chimeric guide endonuclease molecule and a target nucleic acid is provided, and cleavage of the target nucleic acid by the chimeric guide endonuclease molecule is monitored. Cleavage by the chimeric guide molecule corresponds to binding of the guide domain to the target nucleic acid, or to a protein associated with the nucleic acid. The methods of the invention are adapted to cleavage of target nucleic acids, amplification of target nucleic acids, detection of target nucleic acids, screening of genomic target nucleic acid sequences for guide binding domains, and screening for modulators of chimeric guide binding domain activity. Also provided are methods for detecting interactions between other molecules, including hormones

and receptors, enzymes and substrates, and the like.

27 Claims, 9 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 9

---------- KWIC ---------

Detailed Description Text - DETX (99):

Common guide domains include **transcription factors (activators), silencers, nuclear receptors, general transcription** machinery and modifiers of these factors, oncogenes (e.g., myc, jun, fos, myb, max, mad, rel, ets, bcl, myb, mos family members etc.), tumor promoters, metastasis and invasiveness promoters or suppressors and their associated factors and modifiers; tumor suppressors (e.g. p53, WT1, MDM2, Rb family) and their associated factors and modifiers; DNA repair enzymes and their associated factors and modifiers; DNA rearrangement enzymes and their associated factors and modifiers, cell cycle proteins and their associated factors and modifiers; chromatin associated proteins and their modifiers (e.g., kinases, acetylases and deacetylases); DNA modifying enzymes (e.g., **methyltransferases,** topoisomerases, helicases, ligases, kinases, phosphatases, polymerases) and their associated factors and modifiers; RNA modifying enzymes and their associated factors and modifiers, RNA binding factors (directly or indirectly) and their associated factors and modifiers, factors that control chromatin, DNA, RNA and RNP (ribonuclear protein) structure, movement and localization and their associated factors and modifiers; factors derived from microbes (e.g., prokaryotes, eukaryotes and virus) and factors that associate with or modify them.

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FILE 'BIOTECHDS'
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         21115 ACTIVAT?
            50 COACTIVAT?
L40       1275 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'BIOSIS'
        226192 TRANSCRIPTION?
        639090 ACTIVAT?
          3623 COACTIVAT?
L41      40559 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'EMBASE'
        194932 TRANSCRIPTION?
        539367 ACTIVAT?
          3139 COACTIVAT?
L42      31647 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'HCAPLUS'
        254771 TRANSCRIPTION?
       1062699 ACTIVAT?
          4132 COACTIVAT?
L43      52459 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)
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FILE 'NTIS'
          2399 TRANSCRIPTION?
         27539 ACTIVAT?
            92 COACTIVAT?
L44          249 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'ESBIOBASE'
        113012 TRANSCRIPTION?
        240480 ACTIVAT?
          2549 COACTIVAT?
L45       24306 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'BIOTECHNO'
        162026 TRANSCRIPTION?
        221121 ACTIVAT?
          2066 COACTIVAT?
L46       25489 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

FILE 'WPIDS'
         11499 TRANSCRIPTION?
        221394 ACTIVAT?
           269 COACTIVAT?
L47        1255 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

TOTAL FOR ALL FILES
L48      274561 TRANSCRIPTION?(10A)(ACTIVAT? OR COACTIVAT?)

=> s (l36 or l48)(10a)methyltransferase#
FILE 'MEDLINE'
         14273 METHYLTRANSFERASE#
L49         25 (L25 OR L37)(10A)METHYLTRANSFERASE#

FILE 'SCISEARCH'
         10594 METHYLTRANSFERASE#
L50         33 (L26 OR L38)(10A)METHYLTRANSFERASE#

FILE 'LIFESCI'
          4117 METHYLTRANSFERASE#
L51         23 (L27 OR L39)(10A)METHYLTRANSFERASE#

FILE 'BIOTECHDS'
           542 METHYLTRANSFERASE#
L52          3 (L28 OR L40)(10A)METHYLTRANSFERASE#

FILE 'BIOSIS'
         11190 METHYLTRANSFERASE#
L53         40 (L29 OR L41)(10A)METHYLTRANSFERASE#

FILE 'EMBASE'
         10946 METHYLTRANSFERASE#
L54         30 (L30 OR L42)(10A)METHYLTRANSFERASE#

FILE 'HCAPLUS'
         13533 METHYLTRANSFERASE#
L55         73 (L31 OR L43)(10A)METHYLTRANSFERASE#

FILE 'NTIS'
            47 METHYLTRANSFERASE#
L56          0 (L32 OR L44)(10A)METHYLTRANSFERASE#

FILE 'ESBIOBASE'
          3775 METHYLTRANSFERASE#
L57         22 (L33 OR L45)(10A)METHYLTRANSFERASE#
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FILE 'BIOTECHNO'
          5151 METHYLTRANSFERASE#
L58         19 (L34 OR L46)(10A)METHYLTRANSFERASE#

FILE 'WPIDS'
           341 METHYLTRANSFERASE#
L59          2 (L35 OR L47)(10A)METHYLTRANSFERASE#

TOTAL FOR ALL FILES
L60        270 (L36 OR L48)(10A) METHYLTRANSFERASE#

=> s (124 or 160) not 2000-2003/py
FILE 'MEDLINE'
       1814740 2000-2003/PY
L61         29 (L13 OR L49) NOT 2000-2003/PY

FILE 'SCISEARCH'
       3425271 2000-2003/PY
L62         35 (L14 OR L50) NOT 2000-2003/PY

FILE 'LIFESCI'
        346068 2000-2003/PY
L63         24 (L15 OR L51) NOT 2000-2003/PY

FILE 'BIOTECHDS'
         65447 2000-2003/PY
L64          0 (L16 OR L52) NOT 2000-2003/PY

FILE 'BIOSIS'
       1866772 2000-2003/PY
L65         36 (L17 OR L53) NOT 2000-2003/PY

FILE 'EMBASE'
       1548459 2000-2003/PY
L66         39 (L18 OR L54) NOT 2000-2003/PY

FILE 'HCAPLUS'
       3439581 2000-2003/PY
L67         44 (L19 OR L55) NOT 2000-2003/PY

FILE 'NTIS'
         56832 2000-2003/PY
L68          0 (L20 OR L56) NOT 2000-2003/PY

FILE 'ESBIOBASE'
        998494 2000-2003/PY
L69         16 (L21 OR L57) NOT 2000-2003/PY

FILE 'BIOTECHNO'
        423776 2000-2003/PY
L70         22 (L22 OR L58) NOT 2000-2003/PY

FILE 'WPIDS'
       3082229 2000-2003/PY
L71          0 (L23 OR L59) NOT 2000-2003/PY

TOTAL FOR ALL FILES
L72        245 (L24 OR L60) NOT 2000-2003/PY

=> dup rem l72
PROCESSING COMPLETED FOR L72
L73         77 DUP REM L72 (168 DUPLICATES REMOVED)
```

=> d tot

L73 ANSWER 1 OF 77 MEDLINE on STN
TI How chromatin changes its shape.
SO SCIENCE, (1999 Aug 20) 285 (5431) 1200-1, 1203.
Journal code: 0404511. ISSN: 0036-8075.
AU Hagmann M
AN 1999408060 MEDLINE

L73 ANSWER 2 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Mammalian gene CRX characterization and applications for the detection and treatment of retinal degenerative disease
SO PCT Int. Appl., 147 pp.
CODEN: PIXXD2
IN Freund, Carol L.; McInnes, Roderick R.; Looser, Jens; Cepko, Constance L.; Furukawa, Takahisa; Morrow, Eric M.
AN 1999:350679 HCAPLUS
DN 131:1463

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9925721	A1	19990527	WO 1998-US24322	19981113
W: AU, CA, JP, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9914089	A1	19990607	AU 1999-14089	19981113

L73 ANSWER 3 OF 77 MEDLINE on STN DUPLICATE 1
TI Inhibition of DNA **methyltransferase** stimulates the expression of signal transducer and **activator** of **transcription** 1, 2, and 3 genes in colon tumor cells.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1999 Nov 23) 96 (24) 14007-12.
Journal code: 7505876. ISSN: 0027-8424.
AU Karpf A R; Peterson P W; Rawlins J T; Dalley B K; Yang Q; Albertsen H; Jones D A
AN 2000040667 MEDLINE

L73 ANSWER 4 OF 77 MEDLINE on STN DUPLICATE 2
TI Unusual sites of arginine methylation in Poly(A)-binding protein II and in vitro methylation by protein **arginine methyltransferases** PRMT1 and PRMT3.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 May 7) 274 (19) 13229-34.
Journal code: 2985121R. ISSN: 0021-9258.
AU Smith J J; Rucknagel K P; Schierhorn A; Tang J; Nemeth A; Linder M; Herschman H R; Wahle E
AN 1999240708 MEDLINE

L73 ANSWER 5 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Analysis of mice carrying targeted mutations of the glucocorticoid receptor gene argues against an essential role of glucocorticoid signalling for generating adrenal chromaffin cells
SO Development (Cambridge, United Kingdom) (1999), 126(13), 2935-2944
CODEN: DEVPED; ISSN: 0950-1991
AU Finotto, Susetta; Krieglstein, Kerstin; Schober, Andreas; Deimling, Frauke; Lindner, Karin; Bruhl, Barbara; Beier, Konstantin; Metz, Jurgen; Garcia-Arraras, Jose E.; Roig-Lopez, Jose L.; Monaghan, Paula; Schmid, Wolfgang; Cole, Timothy J.; Kellendonk, Christoph; Tronche, Francois; Schutz, Gunther; Unsicker, Klaus
AN 1999:492464 HCAPLUS
DN 131:252700

L73 ANSWER 6 OF 77 MEDLINE on STN DUPLICATE 3
TI Regulation of transcription by a protein methyltransferase.
SO SCIENCE, (1999 Jun 25) 284 (5423) 2174-7.

Journal code: 0404511. ISSN: 0036-8075.
AU Chen D; Ma H; Hong H; Koh S S; Huang S M; Schurter B T; Aswad D W; Stallcup M R
AN 1999316081 MEDLINE

L73 ANSWER 7 OF 77 MEDLINE on STN DUPLICATE 4
TI S-Adenosylmethionine-dependent methylation in Saccharomyces cerevisiae. Identification of a novel protein **arginine methyltransferase**.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jan 8) 274 (2) 814-24.
Journal code: 2985121R. ISSN: 0021-9258.
AU Niewmierzycka A; Clarke S
AN 1999091619 MEDLINE

L73 ANSWER 8 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Activation of human O6-methylguanine-DNA methyltransferase gene by glucocorticoid hormone
SO Oncogene (1999), 18(2), 525-532
CODEN: ONCNES; ISSN: 0950-9232
AU Biswas, Tapan; Ramana, Chilakamarti V.; Srinivasan, Ganesan; Boldogh, Istvan; Hazra, Tapas K.; Chen, Zhenping; Tano, Keizo; Thompson, E. Brad; Mitra, Sankar
AN 1999:117843 HCAPLUS
DN 130:276964

L73 ANSWER 9 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI RNase treatment of yeast and mammalian cell extracts affects in vitro substrate methylation by type I protein arginine N-methyltransferases
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (7 JUN 1999) Vol. 259, No. 2, pp. 391-400.
Publisher: ACADEMIC PRESS INC, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495.
ISSN: 0006-291X.
AU Frankel A; Clarke S (Reprint)
AN 1999:478606 SCISEARCH

L73 ANSWER 10 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
TI [Mechanisms of BTG2 activity, a transcriptional target of p53: Evidences and hypothesis].
MECANISMES D'ACTION DE BTG2, **GENE** CIBLE DE P53: DONNEES ACQUISES ET HYPOTHESES.
SO Bulletin du Cancer, (1999) 86/4 (358-364).
Refs: 42
ISSN: 0007-4551 CODEN: BUCABS
AU Puisieux A.; Magaud J.-P.
AN 1999174896 EMBASE

L73 ANSWER 11 OF 77 MEDLINE on STN DUPLICATE 5
TI Arginine methylation and binding of Hrp1p to the efficiency element for mRNA 3'-end formation.
SO RNA, (1999 Feb) 5 (2) 272-80.
Journal code: 9509184. ISSN: 1355-8382.
AU Valentini S R; Weiss V H; Silver P A
AN 1999146783 MEDLINE

L73 ANSWER 12 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI Identification and characterization of a novel mammalian CpG binding **transcriptional activator** that shares a motif with DNA **methyltransferase** and HRX proteins.
SO EXPERIMENTAL HEMATOLOGY, (JUL 1999) Vol. 27, No. 7, Supp. [1], pp. 61-61.
Publisher: ELSEVIER SCIENCE INC, 655 AVENUE OF THE AMERICAS, NEW YORK, NY 10010.
ISSN: 0301-472X.
AU Voo K S (Reprint); Carlone D L; Jacobsen B M; Flodin A; Skalnik D G

AN 1999:528880 SCISEARCH

L73 ANSWER 13 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Neural regulation of phenylethanolamine N-methyltransferase (PNMT) gene expression in bovine chromaffin cells differs from other catecholamine enzyme genes
SO Journal of Molecular Neuroscience (1999), 12(1), 53-68
CODEN: JMNEES; ISSN: 0895-8696
AU Lee, Ying-Shuan Eda; Raia, Gabrielle; Tonshoff, Christianne; Evinger, Marian J.
AN 1999:592097 HCAPLUS
DN 131:347371

L73 ANSWER 14 OF 77 MEDLINE on STN DUPLICATE 6
TI delta-N-methylarginine is a novel posttranslational modification of arginine residues in yeast proteins.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Nov 6) 273 (45) 29283-6.
Journal code: 2985121R. ISSN: 0021-9258.
AU Zobel-Thropp P; Gary J D; Clarke S
AN 1999009026 MEDLINE

L73 ANSWER 15 OF 77 MEDLINE on STN DUPLICATE 7
TI Identification of protein-arginine N-methyltransferase as 10-formyltetrahydrofolate dehydrogenase.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Oct 16) 273 (42) 27374-82.
Journal code: 2985121R. ISSN: 0021-9258.
AU Kim S; Park G H; Joo W A; Paik W K; Cook R J; Williams K R
AN 1998438510 MEDLINE

L73 ANSWER 16 OF 77 MEDLINE on STN DUPLICATE 8
TI PRMT 3, a type I protein arginine N-methyltransferase that differs from PRMT1 in its oligomerization, subcellular localization, substrate specificity, and regulation.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Jul 3) 273 (27) 16935-45.
Journal code: 2985121R. ISSN: 0021-9258.
AU Tang J; Gary J D; Clarke S; Herschman H R
AN 1998307932 MEDLINE

L73 ANSWER 17 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI C-Fos deficiency inhibits induction of mRNA for some, but not all, neurotransmitter biosynthetic enzymes by immobilization stress
SO Journal of Neurochemistry (1998), 70(5), 1935-1940
CODEN: JONRA9; ISSN: 0022-3042
AU Serova, Lidia I.; Saez, Enrique; Spiegelman, Bruce M.; Sabban, Esther L.
AN 1998:270959 HCAPLUS
DN 129:26592

L73 ANSWER 18 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
DUPLICATE 9
TI Enzymatic methylation of recombinant TIS21 protein-arginine residues.
SO Biochemistry and Molecular Biology International, (1998) 45/5 (871-878).
Refs: 26
ISSN: 1039-9712 CODEN: BMBIES
AU Lim I.K.; Park T.-J.; Kim S.; Lee H.W.; Paik W.K.
AN 1998311260 EMBASE

L73 ANSWER 19 OF 77 LIFESCI COPYRIGHT 2003 CSA on STN DUPLICATE 10
TI p53 is involved in regulation of the DNA repair gene O super(6)-methylguanine-DNA methyltransferase (MGMT) by DNA damaging agents
SO Oncogene, (19980820) vol. 17, no. 7, pp. 845-851.
ISSN: 0950-9232.
AU Grombacher, T.; Eichhorn, U.; Kaina, B.*
AN 1999:12996 LIFESCI

L73 ANSWER 20 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI The 4S benzo(a)pyrene-binding protein is not a transcriptional activator of Cyp1a1 gene in Ah receptor-deficient (AHR -/-) transgenic mice
SO Archives of Biochemistry and Biophysics (1998), 349(2), 349-355
CODEN: ABBIA4; ISSN: 0003-9861
AU Foussat, Julie; Costet, Philippe; Galtier, Pierre; Pineau, Thierry; Lesca, Pierre
AN 1998:53563 HCAPLUS
DN 128:163820

L73 ANSWER 21 OF 77 MEDLINE on STN DUPLICATE 11
TI Identification and characterization of two putative human **arginine methyltransferases** (HRMT1L1 and HRMT1L2).
SO GENOMICS, (1998 Mar 15) 48 (3) 330-40.
Journal code: 8800135. ISSN: 0888-7543.
AU Scott H S; Antonarakis S E; Lalioti M D; Rossier C; Silver P A; Henry M F
AN 1998207248 MEDLINE

L73 ANSWER 22 OF 77 MEDLINE on STN DUPLICATE 12
TI Phenylethanolamine N-methyltransferase gene expression: synergistic activation by Egr-1, AP-2 and the glucocorticoid receptor.
SO BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (1998 Oct 30) 61 (1-2) 154-61.
Journal code: 8908640. ISSN: 0169-328X.
AU Wong D L; Siddall B J; Ebert S N; Bell R A; Her S
AN 1999013984 MEDLINE

L73 ANSWER 23 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI RNA and protein interactions modulated by protein arginine methylation
SO Progress in Nucleic Acid Research and Molecular Biology (1998), 61, 65-131
CODEN: PNMBAF; ISSN: 0079-6603
AU Gary, Jonathan D.; Clarke, Steven
AN 1999:1415 HCAPLUS
DN 130:193393

L73 ANSWER 24 OF 77 MEDLINE on STN DUPLICATE 13
TI Protein N-arginine methylation in adenosine dialdehyde-treated lymphoblastoid cells.
SO ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1998 Mar 1) 351 (1) 53-9.
Journal code: 0372430. ISSN: 0003-9861.
AU Li C; Ai L S; Lin C H; Hsieh M; Li Y C; Li S Y
AN 1998162641 MEDLINE

L73 ANSWER 25 OF 77 MEDLINE on STN DUPLICATE 14
TI Construction of a 2.5-Mb integrated physical and **gene** map of distal 21q22.3.
SO GENOMICS, (1998 Apr 1) 49 (1) 1-13.
Journal code: 8800135. ISSN: 0888-7543.
AU Lapenta V; Sossi V; Gosset P; Vayssettes C; Vitali T; Rabatel N; Tassone F; Blouin J L; Scott H S; Antonarakis S E; Creau N; Brahe C
AN 1998234538 MEDLINE

L73 ANSWER 26 OF 77 MEDLINE on STN DUPLICATE 15
TI Identification of N(G)-methylarginine residues in human heterogeneous RNP protein A1: Phe/Gly-Gly-Gly-Arg-Gly-Gly-Gly/Phe is a preferred recognition motif.
SO BIOCHEMISTRY, (1997 Apr 29) 36 (17) 5185-92.
Journal code: 0370623. ISSN: 0006-2960.
AU Kim S; Merrill B M; Rajpurohit R; Kumar A; Stone K L; Papov V V; Schneiders J M; Szer W; Wilson S H; Paik W K; Williams K R
AN 97282571 MEDLINE

L73 ANSWER 27 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI A putative leucine zipper activator of Pasteurella haemolytica leukotoxin transcription and the potential for modulation of its synthesis by

slipped-strand mispairing
SO Infection and Immunity (1997), 65(9), 3970-3975
CODEN: INFIBR; ISSN: 0019-9567
AU Highlander, Sarah K.; Hang, Vinh T.
AN 1997:596469 HCAPLUS
DN 127:315461

L73 ANSWER 28 OF 77 MEDLINE on STN DUPLICATE 16
TI Detection of weakly expressed genes in the rostral ventrolateral medulla of the rat using micropunch and reverse transcription-polymerase chain reaction techniques.
SO CLINICAL AND EXPERIMENTAL PHARMACOLOGY AND PHYSIOLOGY, (1997 Sep-Oct) 24 (9-10) 755-9.
Journal code: 0425076. ISSN: 0305-1870.
AU Comer A M; Yip S; Lipski J
AN 97461017 MEDLINE

L73 ANSWER 29 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI Biological methylation of myelin basic protein: Enzymology and biological significance
SO INTERNATIONAL JOURNAL OF BIOCHEMISTRY & CELL BIOLOGY, (MAY 1997) Vol. 29, No. 5, pp. 743-751.
Publisher: PERGAMON-ELSEVIER SCIENCE LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON, OXFORD, ENGLAND OX5 1GB.
ISSN: 1357-2725.
AU Kim S; Lim I K; Park G H; Paik W K (Reprint)
AN 97:582049 SCISEARCH

L73 ANSWER 30 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Identification and mapping of a novel human **gene**, HRMT1L1, homologous to the rat protein arginine N-methyltransferase 1 (PRMT1) **gene**
SO Mammalian Genome (1997), 8(7), 526-529
CODEN: MAMGEC; ISSN: 0938-8990
AU Katsanis, Nicholas; Yaspo, Marie-Laure; Fisher, Elizabeth M.C.
AN 1997:466667 HCAPLUS
DN 127:131780

L73 ANSWER 31 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
DUPLICATE 17
TI Human erythrocyte protein L-isoaspartyl methyltransferase: Heritability of basal activity and genetic polymorphism for thermal stability.
SO Archives of Biochemistry and Biophysics, (1997) 346/2 (277-286).
Refs: 47
ISSN: 0003-9861 CODEN: ABBIA4
AU David C.L.; Szumlanski C.L.; DeVry C.G.; Park-Hah J.O.; Clarke S.; Weinshilboum R.M.; Aswad D.W.
AN 97315267 EMBASE

L73 ANSWER 32 OF 77 MEDLINE on STN DUPLICATE 18
TI A protein-**arginine methyltransferase** binds to the intracytoplasmic domain of the IFNAR1 chain in the type I interferon receptor.
SO EMBO JOURNAL, (1997 Jan 15) 16 (2) 260-6.
Journal code: 8208664. ISSN: 0261-4189.
AU Abramovich C; Yakobson B; Chebath J; Revel M
AN 97180929 MEDLINE

L73 ANSWER 33 OF 77 MEDLINE on STN DUPLICATE 19
TI The mammalian immediate-early TIS21 protein and the leukemia-associated BTG1 protein interact with a protein-arginine N-methyltransferase.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Jun 21) 271 (25) 15034-44.
Journal code: 2985121R. ISSN: 0021-9258.
AU Lin W J; Gary J D; Yang M C; Clarke S; Herschman H R

AN 96278999 MEDLINE

L73 ANSWER 34 OF 77 MEDLINE on STN DUPLICATE 20
TI The essential yeast RNA binding protein Np13p is methylated.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1996 Nov 26) 93 (24) 13641-6.
Journal code: 7505876. ISSN: 0027-8424.
AU Siebel C W; Guthrie C
AN 97098447 MEDLINE

L73 ANSWER 35 OF 77 MEDLINE on STN DUPLICATE 21
TI The predominant protein-**arginine methyltransferase** from Saccharomyces cerevisiae.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 May 24) 271 (21) 12585-94.
Journal code: 2985121R. ISSN: 0021-9258.
AU Gary J D; Lin W J; Yang M C; Herschman H R; Clarke S
AN 96218186 MEDLINE

L73 ANSWER 36 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN DUPLICATE 22
TI HUMAN BREAST-CANCER PROGRESSION CAN BE REGULATED BY DOMINANT TRANS-ACTING FACTORS IN SOMATIC-CELL HYBRIDIZATION STUDIES
SO CANCER RESEARCH, (01 AUG 1996) Vol. 56, No. 15, pp. 3560-3569.
ISSN: 0008-5472.
AU SAFARIANS S; STERNLICHT M D; YAMANISHI D T; LOVE S M; BARSKY S H (Reprint)
AN 96:558974 SCISEARCH

L73 ANSWER 37 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Glucocorticoid control of phenylethanolamine N-methyltransferase gene expression: Implications for stress and disorders of the stress axis
SO Stress: Molecular Genetic and Neurobiological Advances, Proceedings of the International Symposium on Catecholamines and Other Neurotransmitters in Stress, 6th, Smolenice Castle, Slovakia, June 19-24, 1995 (1996), Meeting Date 1995, Volume 2, 677-693. Editor(s): McCarty, Richard. Publisher: Harwood, Amsterdam, Neth.
CODEN: 63WCA9
AU Wong, D. L.; Ebert, S. N.; Morita, K.
AN 1997:29975 HCAPLUS
DN 126:99505

L73 ANSWER 38 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN DUPLICATE 23
TI STRESS RESPONSES IN ALFALFA (MEDICAGO-SATIVA L) .20. TRANSCRIPTIONAL ACTIVATION OF PHENYLPROPANOID PATHWAY GENES IN ELICITOR-INDUCED CELL-SUSPENSION CULTURES
SO PLANT MOLECULAR BIOLOGY, (FEB 1996) Vol. 30, No. 3, pp. 427-438.
ISSN: 0167-4412.
AU NI W T; FAHRENDORF T; BALLANCE G M; LAMB C J; DIXON R A (Reprint)
AN 96:265329 SCISEARCH

L73 ANSWER 39 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Regulation of the Serratia marcescens extracellular nuclease: positive control by a homolog of P2 Ogr encoded by a cryptic prophage
SO Journal of Molecular Biology (1996), 256(2), 264-78
CODEN: JMOBAK; ISSN: 0022-2836
AU Jin, Shida; Chen, Yi-chi; Christie, Gail E.; Benedik, Michael J.
AN 1996:120396 HCAPLUS
DN 124:195763

L73 ANSWER 40 OF 77 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Isolation and mapping of two human **genes** homologues (hHMT1 and hHMT2) to a yeast **arginine methyltransferase**.
SO American Journal of Human Genetics, (1996) Vol. 59, No. 4 SUPPL., pp. A159.
Meeting Info.: 46th Annual Meeting of the American Society of Human Genetics San Francisco, California, USA October 29-November 2, 1996

ISSN: 0002-9297.
AU Scott, H. S. (1); Henry, M. F.; Lalioti, M. D. (1); Rossier, C. (1); Silver, P. A.; Antonarakis, S. E. (1)
AN 1996:555880 BIOSIS

L73 ANSWER 41 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Differential activation of the rat phenylethanolamine N-methyltransferase gene by Sp1 and Egr-1
SO Journal of Biological Chemistry (1995), 270(29), 17299-305
CODEN: JBCHA3; ISSN: 0021-9258
AU Ebert, Steven N.; Wong, Dona L.
AN 1995:707848 HCAPLUS
DN 123:162354

L73 ANSWER 42 OF 77 MEDLINE on STN DUPLICATE 24
TI Transcriptional activation of the Epstein-Barr virus latency C promoter after 5-azacytidine treatment: evidence that demethylation at a single CpG site is crucial.
SO MOLECULAR AND CELLULAR BIOLOGY, (1995 Nov) 15 (11) 6150-9.
Journal code: 8109087. ISSN: 0270-7306.
AU Robertson K D; Hayward S D; Ling P D; Samid D; Ambinder R F
AN 96025995 MEDLINE

L73 ANSWER 43 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN DUPLICATE 25
TI **TRANSCRIPTIONAL ACTIVATION** OF THE PHENYLETHANOLAMINE N-**METHYLTRANSFERASE** GENE BY EGR-1 AND SP1
SO JOURNAL OF NEUROCHEMISTRY, (1995) Vol. 65, Supp. S, pp. S77.
ISSN: 0022-3042.
AU WONG D L (Reprint); EBERT S N
AN 95:640264 SCISEARCH

L73 ANSWER 44 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN DUPLICATE 26
TI Structural specificity of substrate for S-adenosylmethionine:protein arginine N-methyltransferases.
SO Biochimica et Biophysica Acta - Protein Structure and Molecular Enzymology, (1995) 1248/1 (11-18).
ISSN: 0167-4838 CODEN: BBAEDZ
AU Rawal N.; Rajpurohit R.; Lischwe M.A.; Williams K.R.; Paik W.K.; Kim S.
AN 95103187 EMBASE

L73 ANSWER 45 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Egr-1 activation of rat adrenal phenylethanolamine N-methyltransferase gene
SO Journal of Biological Chemistry (1994), 269(33), 20885-98
CODEN: JBCHA3; ISSN: 0021-9258
AU Ebert, Steven N.; Balt, Steven L.; Hunter, Joan P. B.; Gashler, Andrea; Sukhatme, Vikas; Wong, Dona L.
AN 1994:550482 HCAPLUS
DN 121:150482

L73 ANSWER 46 OF 77 MEDLINE on STN DUPLICATE 27
TI Peptides with **sequences** similar to glycine, arginine-rich motifs in proteins interacting with RNA are efficiently recognized by methyltransferase(s) modifying arginine in numerous proteins.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1993 May 15) 268 (14) 10501-9.
Journal code: 2985121R. ISSN: 0021-9258.
AU Najbauer J; Johnson B A; Young A L; Aswad D W
AN 93252938 MEDLINE

L73 ANSWER 47 OF 77 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Phenylethanol amine N-**methyltransferase** gene activation: EGR-1 and **glucocorticoid receptor** synergy.
SO Society for Neuroscience Abstracts, (1993) Vol. 19, No. 1-3, pp. 1692.

Meeting Info.: 23rd Annual Meeting of the Society for Neuroscience Washington, D.C., USA November 7-12, 1993
ISSN: 0190-5295.
AU Wong, D. L.; Ebert, S. N.; Balt, S. L.; Hunter, J. P. B.
AN 1994:48315 BIOSIS

L73 ANSWER 48 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI EGR-1, A TRANSCRIPTIONAL REGULATOR OF PHENYLETHANOLOAMINE N-**METHYLTRANSFERASE** GENE-EXPRESSION - SYNERGISTIC EFFECTS WITH THE **GLUCOCORTICOID RECEPTOR**
SO NEUROPSYCHOPHARMACOLOGY, (SEP 1993) Vol. 9, No. 2, Supp. S, pp. S83-S84.
ISSN: 0893-133X.
AU WONG D L (Reprint); EBERT S N; HUNTER J; GASHER A; SUKHATME V P
AN 93:542475 SCISEARCH

L73 ANSWER 49 OF 77 MEDLINE on STN DUPLICATE 28
TI Adrenal phenylethanolamine N-**methyltransferase** induction in relation to **glucocorticoid receptor** dynamics: evidence that acute exposure to high cortisol levels is sufficient to induce the enzyme.
SO JOURNAL OF NEUROCHEMISTRY, (1992 May) 58 (5) 1853-62.
Journal code: 2985190R. ISSN: 0022-3042.
AU Betito K; Diorio J; Meaney M J; Boksa P
AN 92218934 MEDLINE

L73 ANSWER 50 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI STUDIES ON N(G)-METHYLARGININE DERIVATIVES IN MYELIN BASIC-PROTEIN FROM DEVELOPING AND MUTANT **MOUSE**-BRAIN
SO BIOCHEMICAL JOURNAL, (01 NOV 1992) Vol. 287, Part 3, pp. 929-935.
ISSN: 0264-6021.
AU RAWAL N; LEE Y J; PAIK W K; KIM S (Reprint)
AN 92:653725 SCISEARCH

L73 ANSWER 51 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN DUPLICATE 29
TI A REGION OF THE ADA DNA-REPAIR PROTEIN REQUIRED FOR THE ACTIVATION OF ADA TRANSCRIPTION IS NOT NECESSARY FOR ACTIVATION OF ALKA
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1991) Vol. 88, No. 20, pp. 9001-9005.
AU SHEVELL D E; WALKER G C (Reprint)
AN 91:573137 SCISEARCH

L73 ANSWER 52 OF 77 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI MOLECULAR ANALYSIS OF BACILLUS-SUBTILIS ADA MUTANTS DEFICIENT IN THE ADAPTIVE RESPONSE TO SIMPLE ALKYLATING AGENTS.
SO J BACTERIOL, (1991) 173 (24), 7834-7840.
CODEN: JOBAAY. ISSN: 0021-9193.
AU MOROHOSHI F; HAYASHI K; MUNAKATA N
AN 1992:95704 BIOSIS

L73 ANSWER 53 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI ENZYMATIC METHYLATION OF MYELIN BASIC-PROTEIN IN MYELIN
SO BIOCHEMICAL JOURNAL, (1991) Vol. 275, No. APR, pp. 381-387.
AU GHOSH S K; RAWAL N; SYED S K; PAIK W K; KIM S (Reprint)
AN 91:244762 SCISEARCH

L73 ANSWER 54 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI AN ENZYME-LINKED-IMMUNOSORBENT-ASSAY FOR MYELIN BASIC PROTEIN-SPECIFIC PROTEIN METHYLASE-I
SO JOURNAL OF NEUROSCIENCE METHODS, (1991) Vol. 37, No. 2, pp. 133-140.
AU RAWAL N; PAIK W K; KIM S (Reprint)
AN 91:296925 SCISEARCH

L73 ANSWER 55 OF 77 LIFESCI COPYRIGHT 2003 CSA on STN
TI An enzyme-linked immunosorbent assay for myelin basic protein-specific

protein methylase I.
SO J. NEUROSCI. METHODS., (1991) vol. 37, no. 2, pp. 133-140.
AU Rawal, N.; Paik, W.K.; Kim, S.
AN 91:22049 LIFESCI

L73 ANSWER 56 OF 77 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI NEURAL AND HORMONAL REGULATION OF THE TYROSINE HYDROXYLASE GENE IN ADRENAL MEDULLARY CELLS PARTICIPATION OF C-FOS AND AP1 FACTORS.
SO MOL CELL NEUROSCI, (1990) 1 (3), 202-213.
CODEN: MOCNED. ISSN: 1044-7431.
AU STACHOWIAK M K; GOC A; HONG J S; KAPLAN B B; STACHOWIAK E K
AN 1992:30788 BIOSIS

L73 ANSWER 57 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
DUPLICATE 30
TI Substrate specificity for myelin basic protein-specific protein methylase I.
SO Biochimica et Biophysica Acta - Protein Structure and Molecular Enzymology, (1990) 1039/2 (142-148).
ISSN: 0167-4838 CODEN: BBAEDZ
AU Ghosh S.K.; Syed S.K.; Jung S.; Paik W.K.; Kim S.
AN 90183956 EMBASE

L73 ANSWER 58 OF 77 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI SITE-DIRECTED MUTATION OF THE ESCHERICHIA-COLI ADA GENE EFFECTS OF SUBSTITUTION OF METHYL ACCEPTOR CYSTEINE-321 BY HISTIDINE IN ADA PROTEIN.
SO J BACTERIOL, (1989) 171 (3), 1535-1543.
CODEN: JOBAAY. ISSN: 0021-9193.
AU TANO K; BHATTACHARYYA D; FOOTE R S; MURAL R J; MITRA S
AN 1989:227441 BIOSIS

L73 ANSWER 59 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI The glucocorticoid receptor in the adrenal gland is localized in the cytoplasm of adrenaline cells
SO Acta Physiologica Scandinavica (1989), 137(4), 559-60
CODEN: APSCAX; ISSN: 0001-6772
AU Ceccatelli, Sandra; Dagerlind, A.; Schalling, M.; Wikstroem, A. C.; Okret, S.; Gustafsson, J. A.; Goldstein, M.; Hoekfelt, T.
AN 1990:70205 HCAPLUS
DN 112:70205

L73 ANSWER 60 OF 77 MEDLINE on STN DUPLICATE 31
TI Glucocorticoid receptor-immunoreactivity in C1, C2, and C3 adrenergic neurons that project to the hypothalamus or to the spinal cord in the rat.
SO JOURNAL OF COMPARATIVE NEUROLOGY, (1989 Jul 1) 285 (1) 107-16.
Journal code: 0406041. ISSN: 0021-9967.
AU Sawchenko P E; Bohn M C
AN 89327587 MEDLINE

L73 ANSWER 61 OF 77 MEDLINE on STN DUPLICATE 32
TI Morphometrical and microdensitometrical studies on phenylethanolamine-N-**methyltransferase**- and neuropeptide Y-immunoreactive nerve terminals and on **glucocorticoid receptor** -immunoreactive nerve cell nuclei in the paraventricular hypothalamic nucleus in adult and old male rats.
SO NEUROSCIENCE, (1988 Aug) 26 (2) 479-92.
Journal code: 7605074. ISSN: 0306-4522.
AU Zoli M; Agnati L F; Fuxe K; Zini I; Merlo Pich E; Grimaldi R; Harfstrand A; Goldstein M; Wikstrom A C; Gustafsson J A
AN 89015067 MEDLINE

L73 ANSWER 62 OF 77 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
TI MORPHOMETRICAL AND MICRODENSITOMETRICAL STUDIES ON PHENYLETHANOLAMINE-N-**METHYLTRANSFERASE** NERVE AND NEUROPEPTIDE-Y-IMMUNOREACTIVE

NERVE-TERMINALS AND ON **GLUCOCORTICOID RECEPTOR**
-IMMUNOREACTIVE NERVE-CELL NUCLEI IN THE PARAVENTRICULAR HYPOTHALAMIC NUCLEUS IN ADULT AND OLD MALE-RATSI
SO NEUROSCIENCE, (1988) Vol. 26, No. 2, pp. 479-492.
AU ZOLI M; AGNATI L F; FUXE K (Reprint); ZINI I; PICH E M; GRIMALDI R; HARFSTRAND A; GOLDSTEIN M; WIKSTROM A C; GUSTAFSSON J A
AN 88:477823 SCISEARCH

L73 ANSWER 63 OF 77 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI FUNCTIONAL SITES OF THE ADA REGULATORY PROTEIN OF ESCHERICHIA-COLI ANALYSIS BY AMINO ACID SUBSTITUTIONS.
SO J MOL BIOL, (1988) 201 (2), 261-272.
CODEN: JMOBAK. ISSN: 0022-2836.
AU TAKANO K; NAKABEPPU Y; SEKIGUCHI M
AN 1988:330879 BIOSIS

L73 ANSWER 64 OF 77 MEDLINE on STN DUPLICATE 33
TI Glucocorticoid receptor immunoreactivity in monoaminergic neurons of rat brain.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1986 Dec) 83 (24) 9779-83.
Journal code: 7505876. ISSN: 0027-8424.
AU Harfstrand A; Fuxe K; Cintra A; Agnati L F; Zini I; Wikstrom A C; Okret S; Yu Z Y; Goldstein M; Steinbusch H; +
AN 87092331 MEDLINE

L73 ANSWER 65 OF 77 LIFESCI COPYRIGHT 2003 CSA on STN
TI Glucocorticoid receptor immunoreactivity in monoaminergic neurons of rat brain.
SO PROC. NATL. ACAD. SCI. USA., (1986) vol. 83, no. 24, pp. 9779-9783.
AU Haerfstrand, A.; Fuxe, K.; Cintra, A.; Agnati, L.F.; Zini, I.; Wikstroem, A.-C.; Okret, S.; Yu, Z.-Y.; Goldstein, M.; et al..
AN 86:67751 LIFESCI

L73 ANSWER 66 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
TI .beta.-Adrenergic stimulation of protein (**arginine**) **methyltransferase** activity in cultured cerebral cells from embryonic mice.
SO Journal of Neuroscience Research, (1986) 16/2 (377-386).
CODEN: JNREDK
AU Amur S.G.; Shanker G.; Pieringer R.A.
AN 86233852 EMBASE

L73 ANSWER 67 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
TI Correlation between inhibition of myelin basic protein (**arginine**) **methyltransferase** by sinefungin and lack of compact myelin formation in cultures of cerebral cells from embryonic mice.
SO Journal of Neuroscience Research, (1986) 16/2 (367-376).
CODEN: JNREDK
AU Amur S.G.; Shanker G.; Cochran J.M.; et al.
AN 86233851 EMBASE

L73 ANSWER 68 OF 77 LIFESCI COPYRIGHT 2003 CSA on STN DUPLICATE 34
TI Myelin basic protein-specific protein methylase I activity in shiverer mutant **mouse** brain.
SO J. NEUROSCI. RES., (1986) vol. 16, no. 2, pp. 357-365.
AU Kim, S.; Tuck, M.; Ho, L.-L.; Campagnoni, A.T.; Barbarese, E.; Knobler, R.L.; Lublin, F.D.; Chanderkar, L.P.; Paik, W.K.
AN 86:70907 LIFESCI

L73 ANSWER 69 OF 77 MEDLINE on STN DUPLICATE 35
TI **Glucocorticoid receptors** and regulation of phenylethanolamine-N-**methyltransferase** activity in cultured chromaffin cells.

SO JOURNAL OF NEUROSCIENCE, (1985 Aug) 5 (8). 2161-8.
Journal code: 8102140. ISSN: 0270-6474.
AU Kelner K L; Pollard H B
AN 85263810 MEDLINE

L73 ANSWER 70 OF 77 MEDLINE on STN DUPLICATE 36
TI Morphometrical analysis of the distribution of corticotrophin releasing factor, **glucocorticoid receptor** and phenylethanolamine-N-**methyltransferase** immunoreactive structures in the paraventricular hypothalamic nucleus of the rat.
SO NEUROSCIENCE LETTERS, (1985 Mar 15) 54 (2-3) 147-52.
Journal code: 7600130. ISSN: 0304-3940.
AU Agnati L F; Fuxe K; Yu Z Y; Harfstrand A; Okret S; Wikstrom A C; Goldstein M; Zoli M; Vale W; Gustafsson J A
AN 85188868 MEDLINE

L73 ANSWER 71 OF 77 MEDLINE on STN DUPLICATE 37
TI Regulation of myelin basic protein (**arginine**) **methyltransferase** by thyroid hormone in myelinogenic cultures of cells dissociated from embryonic **mouse** brain.
SO JOURNAL OF NEUROCHEMISTRY, (1984 Aug) 43 (2) 494-8.
Journal code: 2985190R. ISSN: 0022-3042.
AU Amur S G; Shanker G; Pieringer R A
AN 84241798 MEDLINE

L73 ANSWER 72 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Glucocorticoid regulation of phenylethanolamine N-methyltransferase (PNMT) in organ culture of superior cervical ganglia
SO Developmental Biology (Orlando, FL, United States) (1984), 105(1), 130-6
CODEN: DEBIAO; ISSN: 0012-1606
AU Bohn, M. C.; Bloom, E.; Goldstein, M.; Black, I. B.
AN 1984:523374 HCAPLUS
DN 101:123374

L73 ANSWER 73 OF 77 MEDLINE on STN DUPLICATE 38
TI The relationship of myelin basic protein (**arginine**) **methyltransferase** to myelination in **mouse** spinal cord.
SO JOURNAL OF NEUROCHEMISTRY, (1982 Jul) 39 (1) 244-7.
Journal code: 2985190R. ISSN: 0022-3042.
AU Crang A J; Jacobson W
AN 82215833 MEDLINE

L73 ANSWER 74 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI The methylation in vitro of myelin basic protein by arginine methylase from **mouse** spinal cord
SO Biochemical Society Transactions (1980), 8(5), 611-12
CODEN: BCSTB5; ISSN: 0300-5127
AU Crang, A. John; Jacobson, W.
AN 1981:78733 HCAPLUS
DN 94:78733

L73 ANSWER 75 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
TI Protein methylation in animal cells. I. Purification and properties of S-adenosyl-L-methionine: Protein(arginine) n.methyltransferase from krebs II ascites cells.
SO Biochimica et Biophysica Acta, (1978) 519/1 (243-254).
CODEN: BBACAQ
AU Casellas P.; Jeanteur P.J.
AN 78375803 EMBASE

L73 ANSWER 76 OF 77 HCAPLUS COPYRIGHT 2003 ACS on STN
TI Effects of carcinogens and other agents on histone methylation in rat liver nuclei by endogenous histone lysine methyltransferase
SO Cancer Research (1974), 34(6), 1424-8

CODEN: CNREA8; ISSN: 0008-5472
AU Baxter, C. Stuart; Byvoet, Paul
AN 1974:459070 HCAPLUS
DN 81:59070

L73 ANSWER 77 OF 77 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
TI Effects of carcinogens and other agents on histone methylation by a histone **arginine methyltransferase** purified from rat liver cytoplasm.
SO Cancer Research, (1974) 34/6 (1418-1423).
CODEN: CNREA8
AU Baxter C.S.; Byvoet P.
AN 75022818 EMBASE

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